

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:27:48 ; Search time 116.174 Seconds
(without alignments)
1245.097 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRIRNTNSESREV.....GKGKSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|---------------------|
| 1 | 1970 | 100.0 | 374 | 2 AAR79165 | Aar79165 Human mon |
| 2 | 1970 | 100.0 | 374 | 4 AAG80107 | Aag80107 Human CCR |
| 3 | 1970 | 100.0 | 374 | 6 ABU09083 | Abu09083 Human che |
| 4 | 1970 | 100.0 | 374 | 7 ADD44861 | Add44861 Human pro |
| 5 | 1970 | 100.0 | 374 | 7 ADD44865 | Add44865 Human pro |
| 6 | 1970 | 100.0 | 374 | 7 ADP65146 | Adp65146 Human che |
| 7 | 1970 | 100.0 | 374 | 8 ADO29221 | Ado29221 Human GPC |
| 8 | 1970 | 100.0 | 374 | 8 ADQ67847 | Adq67847 Human che |
| 9 | 1823 | 92.5 | 344 | 5 ABG92881 | Abg92881 Class I r |
| 10 | 1823 | 92.5 | 344 | 6 ABU61655 | Abu61655 Human mon |
| 11 | 1823 | 92.5 | 344 | 7 ADF72129 | Adf72129 Human G-P |
| 12 | 1823 | 92.5 | 344 | 8 ADP66217 | Adp66217 Human MCP |
| 13 | 1727.5 | 87.7 | 329 | 4 AAB46859 | Aab46859 Human MCP |
| 14 | 1727.5 | 87.7 | 329 | 5 ABB81055 | Abb81055 Human MCP |
| 15 | 1727.5 | 87.7 | 329 | 8 ADRI16266 | Adri16266 Human MCP |
| 16 | 1651.5 | 83.8 | 360 | 2 AAR79166 | Aar79166 Human mon |
| 17 | 1651.5 | 83.8 | 360 | 2 AAW35833 | Aaw35833 Human mon |
| 18 | 1651.5 | 83.8 | 360 | 4 AAG80108 | Aag80108 Human CCR |
| 19 | 1651.5 | 83.8 | 360 | 4 AAU07614 | Aau07614 Human wil |
| 20 | 1651.5 | 83.8 | 360 | 6 ABP97725 | Abp97725 Amino aci |
| 21 | 1651.5 | 83.8 | 360 | 6 ABP81987 | Abp81987 Human C-C |
| 22 | 1651.5 | 83.8 | 360 | 8 ADM67225 | Adm67225 Human adi |
| 23 | 1651.5 | 83.8 | 360 | 8 ADL82831 | Adl82831 Human PRO |
| 24 | 1650.5 | 83.8 | 360 | 4 AAU07613 | Aau07613 Human CCR |
| 25 | 1645.5 | 83.5 | 360 | 4 ABB56340 | Abb56340 Non-endog |

| | | | | | |
|----|--------|------|-----|------------|--------------------|
| 26 | 1589.5 | 80.7 | 347 | 7 ADF56627 | Adf56627 Partial h |
| 27 | 1332.5 | 67.6 | 373 | 8 ADM67224 | Adm67224 Murine ad |
| 28 | 1332.5 | 67.6 | 373 | 8 ADO29222 | Ado29222 Mouse GPC |
| 29 | 1332.5 | 67.6 | 373 | 8 ADP74040 | Adp74040 Murine CC |
| 30 | 1244 | 63.1 | 354 | 8 ADO29228 | Ado29228 Mouse GPC |
| 31 | 1236 | 62.7 | 352 | 4 AAG79089 | Aag79089 Amino aci |
| 32 | 1234 | 62.6 | 354 | 2 AAW54037 | Aaw54037 Mouse CC- |
| 33 | 1230 | 62.4 | 354 | 7 ADD44859 | Add44859 Rat Prote |
| 34 | 1230 | 62.4 | 354 | 7 ADD44863 | Add44863 Rat Prote |
| 35 | 1224 | 62.1 | 352 | 2 AAW27407 | Aaw27407 Human CCR |
| 36 | 1224 | 62.1 | 352 | 2 AAW27123 | Aaw27123 Human che |
| 37 | 1224 | 62.1 | 352 | 2 AAW27125 | Aaw27125 Macaque c |
| 38 | 1224 | 62.1 | 352 | 2 AAW23835 | Aaw23835 Human CC |
| 39 | 1224 | 62.1 | 352 | 2 AAW88232 | Aaw88232 HIV-1 co- |
| 40 | 1224 | 62.1 | 352 | 4 AAE07048 | Aae07048 Human G-p |
| 41 | 1224 | 62.1 | 352 | 4 AAG80111 | Aag80111 Human CCR |
| 42 | 1224 | 62.1 | 352 | 4 AAE04321 | Aae04321 Human che |
| 43 | 1224 | 62.1 | 352 | 4 AAE07039 | Aae07039 Human G-p |
| 44 | 1224 | 62.1 | 352 | 4 AAB46858 | Aab46858 Human HDG |
| 45 | 1224 | 62.1 | 352 | 4 AAB83354 | Aab83354 Human CCR |

ALIGNMENTS

RESULT 1
AAR79165
ID AAR79165 standard; protein; 374 AA.
XX AAR79165;
AC AAR79165;
XX
DT 25-MAR-2003 (revised)
DT 29-DEC-1995 (first entry)
XX
DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.
XX Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..48 /label= extracellular
FT Domain 49..70 /label= transmembrane
FT Domain 80..700 /label= transmembrane
FT Domain 115..136 /label= transmembrane
FT Domain 154..178 /label= transmembrane
FT Domain 204..231 /label= transmembrane
FT Domain 244..268 /label= transmembrane
FT Domain 295..313 /label= transmembrane
FT Domain 314..375 /label= transmembrane
FT Region /label= carboxyl tail
XX WO9519436-A1.
XX
XX 20-JUL-1995.
XX
XX 11-JAN-1995; 95WO-US000476.
XX
XX 13-JAN-1994; 94US-00182962.
XX (REGC) UNIV CALIFORNIA.
XX Charo I, Coughlin S;
XX WPI; 1995-263866/34.
XX

DR N-PSDB; AAQ96297.
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX
 PS Claim 2; Fig 1; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMS7RS orphan receptor (GenBank Accession #M99293). The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pPROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obt'd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obt'd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct FN
 CC field.)
 XX
 SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60
 QY 61 MLVVLILNCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 DB 61 MLVVLILNCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 QY 121 HIGVFGIGFIPIILLTIDRYLAIHVAVPALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 DB 121 HIGVFGIGFIPIILLTIDRYLAIHVAVPALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPFGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240
 DB 181 CQKEDSVYVCGPYFPFGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI 300
 QY 301 NPIIYAVGKPSLFHIALGCRAPLQKPCVCGPGVRPCGNKVKVTTQGLLDCRGKSKI 360
 DB 301 NPIIYAVGKPSLFHIALGCRAPLQKPCVCGPGVRPCGNKVKVTTQGLLDCRGKSKI 360
 QY 361 GRAPEASLQDKEGA 374
 DB 361 GRAPEASLQDKEGA 374

RESULT 2
 AAG80107
 ID AAG80107 standard; protein; 374 AA.

XX
 AC AAG80107;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CCR2a protein.

XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 XX WO200172830-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 02-APR-2001; 2001WO-EP003708.
 XX
 XX 31-MAR-2000; 2000DE-01016013.
 XX
 XX (IPFP-) IPF PHARM GMBH.
 XX (FORS/) FORSSMANN U.
 XX
 XX Forsmann W, Adermann K, Heitland A, Spodsberg N;
 XX WPI; 2001-626256/72.
 XX
 XX Diagnostic agent containing two or more receptor-specific ligands, useful
 XX for detecting tumors, inflammation etc., also therapeutic use of ligand
 XX inhibitors.
 XX
 XX Disclosure; Page 9; 26pp; German.
 XX
 XX This invention describes a novel diagnostic agent (A) comprising at least
 XX two different ligands (I) for receptors (II) that are implicated in
 XX disease. (A) are used for the diagnosis of tumors (especially colorectal
 XX or prostatic), organ rejection, inflammation and autoimmune diseases.
 XX Also inhibitors of (I) are used therapeutically against tumors (and their
 XX metastases), inflammation (particularly bronchial asthma or chronic bowel
 XX inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 XX where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 XX endocrine, motor or urogenital systems or skin are affected, and bone
 XX marrow diseases. The products of the invention are chemokine derivatives
 XX which have cytostatic, antiinflammatory, antiasthmatic,
 XX immunosuppressive, dermatological, antirheumatic, antiarthritic.
 XX Chemokines act on specific tumor and inflammatory cells through a
 XX constellation of chemokine receptors (CR), which control migration and
 XX proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 XX fragments used to illustrate the method of the invention

SQ Sequence 374 AA;
 Query Match 100.0%; Score 1970; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIQAQLPPLYSLVFIFGVGN 60
 QY 61 MLVVLILNCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 DB 61 MLVVLILNCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
 QY 121 HIGVFGIGFIPIILLTIDRYLAIHVAVPALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 DB 121 HIGVFGIGFIPIILLTIDRYLAIHVAVPALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPFGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240
 DB 181 CQKEDSVYVCGPYFPFGNNFHTIMRNILGLVLP LLIMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPPNIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKPSLPHIALGCRAPLOKPVCGPGVPRGKVKVTTQGLDGRGKSKI 360
DB 301 NPIIYAFVGEKPSLPHIALGCRAPLOKPVCGPGVPRGKVKVTTQGLDGRGKSKI 360
QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 3
ABU09083
ID ABU09083 standard; protein; 374 AA.
XX
AC ABU09083;
XX
DT 23-JUL-2003 (first entry)
XX Human chemokine receptor-2 (CCR-2) polypeptide.
XX Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;
KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;
KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;
KW abnormal physiology; abnormal proliferation; degeneration; atrophy;
KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CCR-2.
XX
OS Homo sapiens.
XX
PN US2003018167-A1.
XX
PD 23-JAN-2003.
XX
PF 03-JAN-2002; 2002US-00039659.
XX
PR 05-JUL-1996; 96US-0021664P.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
PR 03-JUL-1997; 97US-00887977.
XX
XX (SCHE) SCHERING CORP.
XX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
XX WPI; 2003-416900/39.
XX
XX New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful
PT for treating conditions associated with abnormal physiology or
PT development, including inflammatory conditions (e.g. asthma), and
PT abnormal proliferation.
XX
PS Disclosure; Page 9-10; 54pp; English.
XX
XX The invention relates to nucleic acids encoding the chemokines TECK, MIP-
CC 3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are
CC useful in isolating DNA clones encoding the chemokines, for generating
CC antibodies, and for predicting oligonucleotides for screening a library
CC to isolate species variants. A nucleic acid encoding a chemokine
CC polypeptide can be used to identify genes, mRNA and cDNA species which
CC encode related or homologous ligands, as well as DNA encoding homologous
CC proteins from different species. The chemokines and antibodies which bind
CC to the polypeptides are useful in the treatment of conditions associated
CC with abnormal physiology or development, including inflammatory
CC conditions such as asthma, abnormal proliferation, regeneration,
CC degeneration and atrophy. This sequence represents the human chemokine
CC receptor-2 (CCR-2) polypeptide, used in the scope of the invention
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFGVGN 60
|||||
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFGVGN 60
61 MLVVLILINCKLCKLUTDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
61 MLVVLILINCKLCKLUTDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
121 HIGYFGGIPFIILLITDRYLAIYHAFVFKARVTFGVVTSVITLVAFAVSPGIIPTK 180
121 HIGYFGGIPFIILLITDRYLAIYHAFVFKARVTFGVVTSVITLVAFAVSPGIIPTK 180
181 CQKEDSVYVCGPYFPRGWNFNHIMENILGLVLPLLIWVICYSGILKTLRCRNEKKRHR 240
181 CQKEDSVYVCGPYFPRGWNFNHIMENILGLVLPLLIWVICYSGILKTLRCRNEKKRHR 240
241 AVRVIPTIMIVYELFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
241 AVRVIPTIMIVYELFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
301 NPIIYAFVGEKPSLPHIALGCRAPLOKPVCGPGVPRGKVKVTTQGLDGRGKSKI 360
301 NPIIYAFVGEKPSLPHIALGCRAPLOKPVCGPGVPRGKVKVTTQGLDGRGKSKI 360
361 GRAPEASLQDKEGA 374
361 GRAPEASLQDKEGA 374

RESULT 4

ADD44861
ID ADD44861 standard; protein; 374 AA.
XX
AC ADD44861;
XX
DT 29-JAN-2004 (first entry)
XX Human Protein P41597, SEQ ID NO 10292.
DE
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P41597.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 374 AA;
 Query Match 100.0%; Score 1970; DB 7; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60
 QY 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPIILLTIDRYLAI VHAFVFAKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
 DB 121 HIGYFGGIFPIILLTIDRYLAI VHAFVFAKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPGGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
 DB 181 CQKEDSVYVCGPYFPGGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLTMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLTMTHCCI 300
 QY 301 NPITIAFVGEKFRSLFHIALGCRAPLQKPVCGPGVVRPGKVKVTTTQGLLDGRGKSI 360
 DB 301 NPITIAFVGEKFRSLFHIALGCRAPLQKPVCGPGVVRPGKVKVTTTQGLLDGRGKSI 360
 QY 361 GRAPEASLQDKEGA 374
 DB 361 GRAPEASLQDKEGA 374

RESULT 5
 ID ADD44865
 ID ADD44865 standard; protein; 374 AA.
 XX
 AC ADD44865;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P41597, SEQ ID NO 10296.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.

XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P41597.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 374 AA;
 Query Match 100.0%; Score 1970; DB 7; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLSLVIFGFGVGN 60
 QY 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPIILLTIDRYLAI VHAFVFAKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
 DB 121 HIGYFGGIFPIILLTIDRYLAI VHAFVFAKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPGGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
 DB 181 CQKEDSVYVCGPYFPGGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLTMTHCCI 300

|||||
241 AVRVFTIMIVYFLFWPPYNNVILLNTFQBFGLSNCESTQSDQATQVTTGLMTHCCI 300
301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVVRPGKVKVTTQGLDGRGKSI 360
301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVVRPGKVKVTTQGLDGRGKSI 360
361 GRAPEASLQDKEGA 374
|||||
361 GRAPEASLQDKEGA 374

RESULT 6
ADP65146
ID ADP65146 standard; protein; 374 AA.
XX AC
XX ADP65146;
DT 12-AUG-2004 (first entry)
XX Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C).
XX autoimmune disease; arthritis; gene expression analysis;
KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;
KW antiarthritic; osteopathic; antigout; anti-inflammatory; dermatological;
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW immune; human.
XX
OS Homo sapiens.
XX
XX WO2003072827-A1.
XX
XX 04-SEP-2003.
XX
XX 31-OCT-2002; 2002WO-US035433.
XX
XX 31-OCT-2001; 2001US-0336220P.
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
XX Hirsch R, Thorton SL;
XX
XX WPI; 2003-712740/67.
XX GENBANK; NP_000638.
XX
XX Diagnosing and analyzing autoimmune disease using gene expression
XX profiles and microarray technology, useful for diagnosing and treating
XX rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
XX gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
XX autoimmune disease or arthritides. The method comprises obtaining a
XX patient sample containing mRNA, analysing gene expression using the mRNA
XX that results in a gene expression signature of the mRNA, and using that
XX gene expression signature to diagnose or analyse the autoimmune disease
XX or arthritides in the patient, where gene expression of at least 60% of
XX the genes correlates with that of the gene signature. The invention
XX further comprises: a treatment of rheumatoid arthritis; identification of
XX genes for targeting in the treatment of rheumatoid arthritis in a mammal
XX other than a mouse; diagnosis of rheumatoid arthritis in a mammal;
XX array or gene chip, specific for rheumatoid arthritis; diagnosis or
XX analyses of autoimmune disease or rheumatoid arthritis; screening the
XX efficacy of a candidate drug in vitro for the treatment of collagen-
XX induced arthritis; and reducing the symptoms associated with collagen-
XX induced arthritis. The compositions of the invention have the following
XX activities: immunosuppressive, anti-rheumatic, antiarthritic, osteopathic,
XX antigout, anti-inflammatory, dermatological, and immunomodulatory. The
XX methods and compositions of the present invention are useful for
XX diagnosing and treating autoimmune disease or arthritides, such as
XX rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
XX Sequence 374 AA;
Query Match 100.0%; Score 1970; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRSRFTIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
DB 1 MLSTSRSRFTIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLITDRYLAI VHAFVAFKARTVTFGVVTSVITLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLITDRYLAI VHAFVAFKARTVTFGVVTSVITLVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWJCYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWJCYSGILKTLRCRNEKKRHR 240
QY 241 AVRVIETIMIVYFLFWPPYNNVILLNTFQBFGLSNCESTQSDQATQVTTGLMTHCCI 300
DB 241 AVRVIETIMIVYFLFWPPYNNVILLNTFQBFGLSNCESTQSDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVVRPGKVKVTTQGLDGRGKSI 360
DB 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVVRPGKVKVTTQGLDGRGKSI 360
QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 7
ADO29221
ID ADO29221 standard; protein; 374 AA.
XX
XX ADO29221;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human GPCR CCR2, SEQ ID NO:322.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
XX cytostatic; anti-inflammatory; vasotropic; antiarrhythmic;
XX CNS; central nervous system; respiratory; antiarrhoeic; antidiabetic;
XX virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
XX Homo sapiens.
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX PA
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 PI N-PSDB; ADO29829.
 XX WPI; 2004-390329/36.
 DR N-PSDB; ADO29829.
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX XX
 PS Claim 151; SEQ ID NO 322; 542pp; English.
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ
 SQ Sequence 374 AA;
 Query Match 100.0%; Score 1970; DB 8; Length 374;
 Best Local Similarity 100.0%; Pred. No. 5.1e-215;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAGLLPPLYSLVIFGFGVN 60
 DB 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAGLLPPLYSLVIFGFGVN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWHAHSANWVFGNACKLFGLY 120
 DB 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWHAHSANWVFGNACKLFGLY 120
 QY 121 HIGVFGIGIFPIILLTIDRYLAIHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTK 180
 DB 121 HIGVFGIGIFPIILLTIDRYLAIHAVFALKARTVFGVTSVITLWVAVFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVLLIMVICYSGLIKTLRCNEKRRH 240

DB 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVLLIMVICYSGLIKTLRCNEKRRH 240
 QY 241 AVRVIETIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSQLDQATQVTTETLGMTHCCI 300
 DB 241 AVRVIETIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSQLDQATQVTTETLGMTHCCI 300
 QY 301 NPIIYAFVGEKFRSLFPHIALGCRAPLQKPVCGGVRPGKVKVVTQTGLDGRGKSKI 360
 DB 301 NPIIYAFVGEKFRSLFPHIALGCRAPLQKPVCGGVRPGKVKVVTQTGLDGRGKSKI 360
 QY 361 GRAPEASLQDKEGA 374
 DB 361 GRAPEASLQDKEGA 374
 RESULT 8
 ADQ67847
 ID ADQ67847 standard; protein; 374 AA.
 XX AC ADQ67847;
 XX DT 07-OCT-2004 (first entry)
 DE Human chemokine receptor CCR-2.
 XX KW Human; receptor; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
 KW chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
 KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
 KW development; inflammatory condition; asthma.
 XX OS Homo sapiens.
 XX PN US2004137578-A1.
 XX PD 15-JUL-2004.
 XX PF 09-JAN-2004; 2004US-00754071.
 XX PR 05-JUL-1996; 96US-0021664P.
 PR 11-OCT-1996; 96US-0028329P.
 PR 04-JUN-1997; 97US-0048593P.
 PR 03-JUL-1997; 97US-00887977.
 PR 03-JAN-2002; 2002US-00039659.
 XX (WANG/) WANG W.
 PA (GISH/) GISH K C.
 PA (SCHA/) SCHALL T J.
 PA (VICA/) VICARI A.
 PA (ZLOT/) ZLOTNIK A.
 XX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
 XX WPI; 2004-533376/51.
 XX New substantially pure or isolated Thymus Expressed Chemokine (TECK),
 PT useful for treating conditions associated with abnormal physiology or
 PT development, including inflammatory conditions, e.g. asthma.
 XX Disclosure; SEQ ID NO 14; 54pp; English.
 XX The invention relates to a substantially pure or isolated polypeptide
 CC comprises the mature protein of human TECK (thymus expressed chemokine)
 CC whose full length sequence appears as ADQ67837. Also included are an
 CC isolated or recombinant nucleic acid encoding mature TECK, an expression
 CC vector comprising the nucleic acid, a host cell comprising the expression
 CC vector and a method for producing the polypeptide. Also disclosed are the
 CC mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta
 CC (and their encoding cDNAs), and the cDNAs and encoded proteins
 CC corresponding to human chemokine receptors DCCR (dendritic cell receptor
 CC for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for
 CC chemokine). The polypeptide is useful for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions, e.g. asthma. The present sequence represents a human

CC chemokine receptor showing sequence similarity to M/DCCR.

XX SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVN 60
Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVN 60
Qy 61 MLVLLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVLLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWLVAFASVPGIIFTK 180
Db 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWLVAFASVPGIIFTK 180
Qy 181 CQKEDSVVCGPYFPFRGNWNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRHR 240
Db 181 CQKEDSVVCGPYFPFRGNWNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLFTWTPYNIIVILLNTFQEPFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFTWTPYNIIVILLNTFQEPFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Qy 301 NPPIYAFVGEKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQTGILLDGRGKSI 360
Db 301 NPPIYAFVGEKFRSLFHIALGCRITAPLQKPVCGGPGVRPGKNVKTQTGILLDGRGKSI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 9
ABG92881
ID ABG92881 standard; peptide; 344 AA.

AC ABG92881;
XX 19-NOV-2002 (first entry)
XX Class I receptors WSXWS motif.
XX Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.
XX Synthetic.
XX WO200264612-A2.
XX 22-AUG-2002.
XX 08-FEB-2002; 2002WO-US003634.
XX 09-FEB-2001; 2001US-00779880.
XX 09-FEB-2001; 2001WO-US004153.
XX 12-JUN-2001; 2001US-0297257P.
XX 08-AUG-2001; 2001US-0310458P.
XX 12-OCT-2001; 2001US-0328447P.
XX 21-DEC-2001; 2001US-0341725P.
XX

(HUMA-) HUMAN GENOME SCI INC.
XX Roschke V, Rosen CA, Ruben SM;
XX WPI; 2002-643455/69.
XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
XX treating, preventing, ameliorating or monitoring diseases or disorders
XX associated with aberrant expression of HDGNR10 e.g. cancer.
XX Example 17; Page 386; 562pp; English.

CC The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.3F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring
CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC sequence of the WSXWS motif found in class I receptors
XX
XX SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVNMLVLLINCKKLCIT 77
Db 1 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVNMLVLLINCKKLCIT 60
Qy 78 DIVLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db .61 DIVLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
Qy 138 RYLAIHAVFALKARTVTFGVTSVITLWLVAFASVPGIIFTKCKEDSVVCGPYFPFRG 197
Db 121 RYLAIHAVFALKARTVTFGVTSVITLWLVAFASVPGIIFTKCKEDSVVCGPYFPFRG 180
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRHRVAVRVIPTIMIVYFLFTW 257
Db 181 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRHRVAVRVIPTIMIVYFLFTW 240
Qy 258 PYNIVILLNTFQEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
Db 241 PYNIVILLNTFQEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300
Qy 318 IALGCRITAPLQKPVCGGPGVRPGKNVKTQTGILLDGRGKSI 361
Db 301 IALGCRITAPLQKPVCGGPGVRPGKNVKTQTGILLDGRGKSI 344

RESULT 10
ABU61655
ID ABU61655 standard; protein; 344 AA.
XX ABU61655;
XX DT 08-AUG-2003 (first entry)

XX DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.
XX KW Human; G-protein chemokine receptor; receptor; HDGMR10; MCP-1;
XX 7-transmembrane receptor; monocyte chemoattractant protein 1.
XX OS Homo sapiens.
XX PN US2003023044-A1.
XX PD 30-JAN-2003.
XX PF 03-SEP-2002; 2002US-00232686.
XX PR 06-JUN-1995; 95US-00466343.
XX PR 18-NOV-1998; 98US-00195662.
XX PR 25-JUN-1999; 99US-00339912.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Li Y, Ruben SM;
XX PI WPI; 2003-456307/43.
XX DR Producing an antibody, involves immunizing an animal with a polypeptide
XX PT or with a polypeptide encoded by the human G-protein chemokine receptor
XX PT clone in ATCC 97183, and recovering the antibody.
XX PS Disclosure; Fig 2; 23pp; English.
XX SQ The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGMR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the monocyte
CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the
CC HDGMR10 polypeptide of the invention
XX SQ Sequence 344 AA;
Query Match 92.5%; Score 1823; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLCLT 77
Db 1 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLCLT 60
Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFILLTID 137
Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFILLTID 120
Qy 138 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVCGPYPPRG 197
Db 121 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVCGPYPPRG 180
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKRRHRAVRVIFIMIVYFLFWT 257
Db 181 WNNFHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKRRHRAVRVIFIMIVYFLFWT 240
Qy 258 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317
Db 241 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 300
Qy 318 IALGCRITAPLQKPVCGGVRPGNRNVKVTITQGLDGRGKSGIS 361
Db 301 IALGCRITAPLQKPVCGGVRPGNRNVKVTITQGLDGRGKSGIS 344
RESULT 11
ADF72129
ID ADF72129 standard; protein; 344 AA.

XX ADF72129;
XX AC 12-FEB-2004 (first entry)
XX DT. Human G-protein chemokine receptor (CCRS) ligand MCP-1.
XX DE cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5;
XX KW cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring;
XX KW cancer; hyperproliferative disorder; human; HDGMR10; ligand; MCP-1.
XX OS Homo sapiens.
XX PN US2003166024-A1.
XX PD 04-SEP-2003.
XX PF 01-MAY-2002; 2002US-00135839.
XX PR 09-FEB-2000; 2000US-0181258P.
XX PR 09-MAR-2000; 2000US-0187999P.
XX PR 22-SEP-2000; 2000US-0234336P.
XX PR 09-FEB-2001; 2001US-00779879.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Roschke V, Li Y, Ruben SM;
XX PI WPI; 2003-898066/82.
XX DR New polypeptide comprising domains of an antibody that binds G-protein
XX PT chemokine receptor CCR5 is useful to detect, diagnose, prognose or
XX PT monitor cancers and other hyperproliferative disorders and to treat or
XX PT prevent a disease or disorder.
XX PS Disclosure; SEQ ID NO 9; 179pp; English.
XX SQ The invention describes a new isolated polynucleotide that encodes an
CC antibody (AB1) comprising an amino acid sequence of at least one, two or
CC three complementarity determining regions (CDR) of a heavy chain variable
CC (VH) domain of an antibody (AB2) that immunospecifically binds to a G-
CC protein chemokine receptor (CCRS), at least one, two or three CDR regions
CC of a light chain variable (VL) domain of AB2 or at least one, two or
CC three CDR regions of both a VH and a VL domain of AB2. The antibody is
CC useful for detecting, diagnosing, prognosing or monitoring cancers and
CC other hyperproliferative disorders and for treating, preventing or
CC ameliorating a disease or disorder. This is the amino acid sequence of
CC MCP-1, a ligand of human G protein chemokine receptor (CCRS) HDGMR10.
XX SQ Sequence 344 AA;
Query Match 92.5%; Score 1823; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 18 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLCLT 77
Db 1 EVVTFDDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGNMVLVLLINCKKLCLT 60
Qy 78 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFILLTID 137
Db 61 DIYLLNLAISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLYHIGYFGGIFILLTID 120
Qy 138 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVCGPYPPRG 197
Db 121 RYLAIHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVVCGPYPPRG 180
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKRRHRAVRVIFIMIVYFLFWT 257
Db 181 WNNFHTIMRNILGLVPLLMVICYSGLIKTLRCRNEKRRHRAVRVIFIMIVYFLFWT 240
Qy 258 PYNIVILLNTFQEPFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317

CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGMR10, (i) are useful for screening for compounds which
 CC activate or inhibit activation of (i). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukaemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGMR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)
 XX
 SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 1.8e-187;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 QY 18 EYVTFDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKKLCCLT 77
 DB 1 EYVTFDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKKLCCLT 60
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLITID 137
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLITID 105
 QY 138 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPPRG 197
 DB 106 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPPRG 165
 QY 198 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKKRHRVAVIFITMIVYFLFWT 257
 DB 166 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKKRHRVAVIFITMIVYFLFWT 225
 QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 317
 DB 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 285
 QY 318 IALGCRAPLQKPVCGGPGVRPGKRVKVTQTQGLLDGRGKSG 361
 DB 286 IALGCRAPLQKPVCGGPGVRPGKRVKVTQTQGLLDGRGKSG 329

RESULT 14
 ABB81055
 ID ABB81055 standard; protein; 329 AA.
 XX
 AC ABB81055;
 XX

DT 05-NOV-2002 (first entry)

DE Human MCP-1 receptor.

XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGMR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antipsoriatic; anti-allergic; anti-inflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.
 XX

OS Homo sapiens.

XX US2002076745-A1.

XX 20-JUN-2002.

XX 18-NOV-1998; 98US-00195662.

XX 06-JUN-1995; 95US-00466343.

XX (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX

PI Li Y, Ruben SM;
 XX WPI; 2002-598724/64.
 DR
 XX New polynucleotide encoding a human G protein chemokine receptor HDGMR10,
 PT useful e.g. for treating tumors.
 PS
 XX Example; Fig 2; 22pp; English.
 CC The invention relates to a novel human 7-transmembrane receptor, HDGMR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGMR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents a human MCP-1 receptor used in
 CC comparison studies with the HDGMR10 receptor
 XX
 SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 5; Length 329;
 Best Local Similarity 95.6%; Pred. No. 1.8e-187;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 QY 18 EYVTFDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKKLCCLT 77
 DB 1 EYVTFDYDYGAPCHKFDVKQIGAOQLPPLYSIVFIQFVGNMVLVLLINCKKLCCLT 60
 QY 78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLITID 137
 DB 61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLITID 105
 QY 138 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPPRG 197
 DB 106 RYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPPRG 165
 QY 198 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKKRHRVAVIFITMIVYFLFWT 257
 DB 166 WNNFHTIMRNILGLVPLLMVLCYSGLIKTLRCNEKKRHRVAVIFITMIVYFLFWT 225
 QY 258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 317
 DB 226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKRSLEH 285
 QY 318 IALGCRAPLQKPVCGGPGVRPGKRVKVTQTQGLLDGRGKSG 361
 DB 286 IALGCRAPLQKPVCGGPGVRPGKRVKVTQTQGLLDGRGKSG 329

RESULT 15
 ADR16266
 ID ADR16266 standard; protein; 329 AA.
 XX

AC ADR16266;

XX 21-OCT-2004 (first entry)

XX Human MCP-1 receptor protein fragment.

XX G-protein chemokine receptor; CCR5; HDGMR10; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; prostaglandin-independent fever;
 KW bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock;
 KW hyper eosinophilic syndrome; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; chronic infection; leukaemia;
 KW autoimmune disease; parasitic infection; psoriasis; human;
 KW MCP-1 receptor; receptor.

XX Homo sapiens.

XX US2004151719-A1.

XX

THIS PAGE IS LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:29:43 ; Search time 25.9864 Seconds
(without alignments)
1384.767 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRSRFRINTNESGEV.....GKGKSGIGRAPEASIQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-----------------------------|
| 1 | 1970 | 100.0 | 374 | 2 | 138450 chemokine (C-C) re |
| 2 | 1651.5 | 83.8 | 360 | 2 | JC2443 chemokine (C-C) re |
| 3 | 1224 | 62.1 | 352 | 2 | A43113 chemokine (C-C) re |
| 4 | 967.5 | 49.1 | 355 | 2 | A45177 chemokine (C-C) re |
| 5 | 960 | 48.7 | 359 | 2 | I49341 Mip-1 alpha recept |
| 6 | 902.5 | 45.8 | 355 | 2 | I49339 macrophage inflam |
| 7 | 890.5 | 45.2 | 355 | 2 | G02436 chemokine (C-C) re |
| 8 | 833 | 42.3 | 360 | 2 | JC4587 chemokine (C-C) re |
| 9 | 831.5 | 42.2 | 360 | 2 | A57160 chemokine (C-C) re |
| 10 | 794.5 | 40.3 | 383 | 2 | S85594 G protein-coupled |
| 11 | 731 | 37.1 | 356 | 2 | I49340 Mip-1 alpha recept |
| 12 | 723 | 36.7 | 355 | 2 | JC5067 G protein-coupled |
| 13 | 704.5 | 35.8 | 354 | 2 | I58186 probable G protein-c |
| 14 | 698 | 35.4 | 355 | 2 | JC4304 orphan G protein-c |
| 15 | 644.5 | 32.7 | 344 | 2 | JC5942 chemokine receptor |
| 16 | 584 | 29.6 | 378 | 2 | B55735 lymphocyte-specifi |
| 17 | 575.5 | 29.2 | 378 | 2 | A55735 G protein-coupled |
| 18 | 570 | 28.9 | 378 | 2 | A45680 G protein-coupled |
| 19 | 554.5 | 28.1 | 369 | 2 | JC5068 G protein-coupled |
| 20 | 541.5 | 27.5 | 360 | 2 | A53611 interleukin-8 rece |
| 21 | 537 | 27.3 | 359 | 2 | A48921 interleukin-8 rece |
| 22 | 531 | 27.0 | 352 | 2 | G00048 fuoin (LESTRA) - c |
| 23 | 530.5 | 26.9 | 353 | 2 | S28787 neuropeptide Y/pep |
| 24 | 529.5 | 26.9 | 355 | 2 | J01231 interleukin-8 rece |
| 25 | 528 | 26.8 | 352 | 2 | A45747 neuropeptide Y/pep |
| 26 | 526 | 26.7 | 358 | 2 | A53752 interleukin-8 rece |
| 27 | 526 | 26.7 | 367 | 2 | J50349 interferon-inducib |
| 28 | 524.5 | 26.6 | 350 | 2 | A39445 interleukin-8 rece |
| 29 | 523 | 26.5 | 356 | 2 | S42096 interleukin-8 rece |

RESULT 1
138450
Chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C:Accession: I38450
R:Charo, I.P.; Myers, S.J.; Heiman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: UNIPROT:P41597; EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:947255
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

| | | | | | | | |
|-----------------------|--------|---------------------|----------------------------------|-------------------------|--------------|-----------|------|
| Query Match | 100.0% | Score | 1970; | DB | 2; | Length | 374; |
| Best Local Similarity | 100.0% | Pred. No. | 1e-164; | | | | |
| Matches | 374; | Conservative | 0; | Mismatches | 0; | Indels | 0; |
| Gaps | 0; | | | | | | |
| Qy | 1 | MLSTSRSRFRINTNESGEV | TTFFDYDGAPCHKFDVKQIGALPLPLYSLVFI | FGVGN | 60 | | |
| Db | 1 | MLSTSRSRFRINTNESGEV | TTFFDYDGAPCHKFDVKQIGALPLPLYSLVFI | FGVGN | 60 | | |
| Qy | 61 | MLVLLILINCKKLC | LDIYLLNLAI | SDLLFLITLPLWAHSAANEVFGN | AMCKLFTGLY | 120 | |
| Db | 61 | MLVLLILINCKKLC | LDIYLLNLAI | SDLLFLITLPLWAHSAANEVFGN | AMCKLFTGLY | 120 | |
| Qy | 121 | HIGYFGGIFP | ILLITIDRYLAIVHAFAL | KARTVTFGVT | SVITLWVAFASV | PGIIFTK | 180 |
| Db | 121 | HIGYFGGIFP | ILLITIDRYLAIVHAFAL | KARTVTFGVT | SVITLWVAFASV | PGIIFTK | 180 |
| Qy | 181 | CKEDSVYVCGPY | PPRGNNFHTIMRNILGLVPL | LLIMVICYS | GILKTL | LCRNEKKRR | 240 |
| Db | 181 | CKEDSVYVCGPY | PPRGNNFHTIMRNILGLVPL | LLIMVICYS | GILKTL | LCRNEKKRR | 240 |

```
Qy 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQAQTQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQAQTQVTTGLMTHCCI 300

Qy 301 NPIIYAVGKFRSLFHIALGCRITAPLOKPVCGGPGVRPGKQNVKVTQGLLDGRGKGS 360
Db 301 NPIIYAVGKFRSLFHIALGCRITAPLOKPVCGGPGVRPGKQNVKVTQGLLDGRGKGS 360

Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2
JC2443
Chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: UNIPROT:P41597; DBJ:J29984; NID:9531246; PIDN:BAA06253.1; PID:G5312
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pr
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: EMBL:1-360 <RES>
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;
Best Local Similarity 95.5%; Pred. No. 7.1e-137;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRFRFTNTNESGEVTTTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVIFGFGVN 60
Db 1 MLSTSRFRFTNTNESGEVTTTFDDYDYGAPCHKFDVKQIQAQLLPPLYSLVIFGFGVN 60

Qy 61 MLVVLILNCKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILNCKLKCLTDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy 121 HIGYFGGIFPIILLTIDRYLAIVAHVPAFKARTVTFGVTTSVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIVAHVPAFKARTVTFGVTTSVITLWVAVPASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPVPFGNNFHTIMRNILGLVPLLTIMVLCYSGLIKTLRCNKKRHR 240
Db 181 CQKEDSVYVCGPVPFGNNFHTIMRNILGLVPLLTIMVLCYSGLIKTLRCNKKRHR 240
```

```
Qy 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQAQTQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSQLDQAQTQVTTGLMTHCCI 300

Qy 301 NPIIYAVGKFR---SLP---HIALG-CRIAPL 327
Db 301 NPIIYAVGKFRYLVSFFPRKHITKRFCQCPV 334

RESULT 3
A43113
Chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:G1262810; PIDN:CAA62796.1; PID:G1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184,'INDSHLGAPAAACHGHLILGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:G1524062; PIDN:CAA67767.1; PID:G1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
J. Leukoc. Biol. 60, 147-152, 1996
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:G1457945; PIDN:AAC50598.1; PID:G1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
A;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
```

A;Note: probably acts to control granulocyte proliferation and differentiation

C;Superfamily: vertebrate rhodopsin

C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran

F;32-56/Domain: transmembrane #status predicted <TM1>

F;67-87/Domain: transmembrane #status predicted <TM2>

F;103-124/Domain: transmembrane #status predicted <TM3>

F;142-166/Domain: transmembrane #status predicted <TM4>

F;193-218/Domain: transmembrane #status predicted <TM5>

F;236-257/Domain: transmembrane #status predicted <TM6>

F;285-300/Domain: transmembrane #status predicted <TM7>

F;20-269,101-178/Disulfide bonds: #status predicted

F;268/Binding site: carboxydrate (Asn) (covalent) #status predicted

F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted

F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;

Best Local Similarity 76.3%; Pred. No. 1.8e-99;

Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCFKFDVKQIGAQLLPPYLSLVIFGFGVGNMLVLLINCKKLCITDIYL 81

DB 10 YDINYVTSBPQKINVKQIAARLLPPYLSLVIFGFGVGNMLVLLINCKKLSMTDIYL 69

QY 82 LNLAISDLLELTPLWAHSAANEWFGNANCKLFTGLYHIGYFGGFIILLITIDRYLA 141

DB 70 LNLAISDLFFLLTVPFWAHYAAQWDFGNTMQLLTGLYFIQFGSGFIILLITIDRYLA 129

QY 142 IYHVAVALKARTVTFGVTSVITLWAVPASVPGIILFTKCKEDSVVVGCPYP---RG 197

DB 130 VYHVAVALKARTVTFGVTSVITWVAVFASLPGIILFTRSQKGLHYTCSHFPYQYQF 189

QY 198 WNNFHTIMRNILGLVLPPLLIMVICYSGLKTLARCRNEKKRHRVRIFTIMIVYLFWT 257

DB 190 WKNFQTLKIVILGLVLPPLLVMVICYSGLKTLARCRNEKKRHRVRLIFTIMIVYLFWA 249

QY 258 PYNIVILLTFQBFGLSNCESTSOLDQATQVTTETLGMTHCCINPIIYAVGKFRSLP- 316

DB 250 PYNIVILLNTFQBFGLNCCSSNRLDQAMQVTTETLGMTHCCINPIIYAVGKFRNYLL 309

QY 317 -----HTA 319

DB 310 VYFQKHIA 317

RESULT 4

A45177

chemokine (C-C) receptor 1 - human

N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A45177; #accession_revision 30-Sep-1993 #text_change 09-Jul-2004

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Accession: A45177

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-355 <NEO>

A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A;Experimental source: HL60 cells

A;Note: sequence extracted from NCBI backbone (NCBIP:124876)

R;Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha

A;Reference number: I55671; MUID:93240122; PMID:7683036

A;Accession: I55671

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-355 <RES>

A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C;Genetics:

A;Gene: GDB:CMKB1; CMKR-1

Qy 129 FFIILLIDRYLAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVY 188
Db 126 FFIILLIDRYLAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVY 185
Qy 189 VCGPYFRPG---WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHVRV 244
Db 186 SCSPRYEGEDSWKRFHRLMNFGLALPLLVNVICYSIGIITKLLRCPN-KKKHKAIRL 244
Qy 245 IFTIMVYFLFWPTNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPIL 304
Db 245 IFVVMIVFFIFWPTNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPIL 304
Qy 305 YAFVGEKFRS---LFHIALGCRAPLQKPVCGPGVRGPKNVKVTTCQGL---LDGRGKG 357
Db 305 YAFVGERFRKHLRFFH-----RNVQPTWENIFQFLPGENG 341
Qy 358 KSTGRAPESLQD 370
Db 342 RTSVSPSTGEQE 354

RESULT 6

I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: UNIPROT:P51675; EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:98815
C:Superfamily: vertebrate rhodopsin

Query Match 45.8%; Score 902.5; DB 2; Length 355;
Best Local Similarity 53.1%; Pred. No. 2.4e-71;
Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;
Qy 21 TTFEDYDYGAPCHKFDVKQIGALLPPLYSIVTFGFGVGNMLVVLILINCKKLCITDIY 80
Db 13 TTFEDYDGSFPCQKTAFAAGALLPPLYSIVTFGFGVGNMLVVLILINCKKLCITDIY 72
Qy 81 LLNLAISSLFLITPLWLA-HSANEVWFGNAMCKLFTGLYHIGYFGIGFIILLITDIDY 139
Db 73 LFNLAISDLVFLFTLPFWIDYKLDWIFGDAMCKLLSGFYTLGLYSEIIFILLITDIDY 132
Qy 140 LAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVYVCGPYFRP--- 195
Db 133 LAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVYVCGPYFRP--- 192
Qy 196 RGNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHVRVFTIMVYFLF 255
Db 193 KQWKRFOALKNLGLILPLLMVICYAGIIRLLR-RPSEKKVAVRLFAITLFLFLL 251
Qy 256 WTPNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPILYAFVGEKFP--- 312
Db 252 WTPNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPILYAFVGEKFP--- 311
Qy 313 -RSLF--HIALGCRAPLQK 329
Db 312 LRQLFORHVAI-----FLAK 326

RESULT 7

G02436
Chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: UNIPROT:P51677; EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477560
R:Combadere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protei
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273, 106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 45.2%; Score 890.5; DB 2; Length 355;
Best Local Similarity 54.6%; Pred. No. 2.7e-70;
Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;
Qy 21 TTFEDYDYGAPCHKFDVKQIGALLPPLYSIVTFGFGVGNMLVVLILINCKKLCITDIY 80
Db 14 TSYD-DVGLCEKADTRALMAQFVPLPPLYSIVTFGFGVGNMLVVLILINCKKLCITDIY 72
Qy 81 LLNLAISSLFLITPLWLAHSA-ANWVWFGNAMCKLFTGLYHIGYFGIGFIILLITDIDY 139
Db 73 LLNLAISSLFLITPLWLAHSA-ANWVWFGNAMCKLFTGLYHIGYFGIGFIILLITDIDY 132
Qy 140 LAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVYVCGPYFRP--- 196
Db 133 LAIVHAFKARTVTFGVVTSVITLWVAFVSGIIFTCKQEDSVYVCGPYFRP--- 192
Qy 197 -GNNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHVRVFTIMVYFLF 255
Db 193 YSRHFFHTLMTFCLVPLLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFFIF 251
Qy 256 WTPNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPILYAFVGEKFRS- 314
Db 252 WTPNYNIVILLNTFOEFGLSNCSTSQLDOATQVETLGHCCINPILYAFVGEKFRS- 311
Qy 315 ---LFH 317
Db 312 LRHFFH 317

RESULT 8

JC4587
Chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: JC4587
R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 219, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to

A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167851
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.3%; Score 833; DB 2; Length 360;
Best Local Similarity 47.9%; Pred. No. 2.9e-65;
Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

Qy 10 IRNTNSESVEVTFDDYD-YGAPCHKFDVKQIGQAQLPPLYSLVPIFGVGNMLVLLI 68
Db 6 VTDITQDETNNYSYFYESMPKCTKGKAFGEVFLPPLYSLVFLGLFGNSVVLVLF 65
Qy 69 NCKKLKLTDLIYLNLAISDLEFLITLPLMAHSAANWVFGNACKLFTGLYHIGYGGI 128
Db 66 KYKRLKSMTDVYLNLAISDLEFLVLSUPFWGYAADQWVFGLGKIVSNMVLVGFYSGI 125
Qy 129 FFIILLITDRYLAIVHAFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVY 188
Db 126 FFIMLSIDRYLAIVHAFVSKARTLYGVTSITLSVAVFASVLPGLLSTCYTEHNHT 185
Qy 189 VCGPYF---PRGWNFHTIMNLIIGLVPLLMIVICYSGILTKLLRCNEKKHRAVRVI 245
Db 186 YCKTQYSVNSTWTKVLSLEINVLGLLPIGLIMLFWYSMIIRTLQHCCKNEK-NRAVRMI 244
Qy 246 FTIMVVFLEWTPNYVILLNTFOEPFLSNCSTSQLDQATQVETGLMTHCCINILY 305
Db 245 FGVLVFLGFPTNYVLLFLETLVEVLDQCTLERYLDVAIQATETLGFTHCCINPVY 304
Qy 306 AFVGEKFR---SLFHIALGRIAPLQKPCVCGP 335
Db 305 FFLGKFRKYYTQLFR-----TCRGP 325

RESULT 9
A57160
Chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R;Power: C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POH>
A;Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g97145
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>

F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5; DB 2; Length 360;
Best Local Similarity 51.9%; Pred. No. 3.9e-65;
Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

Qy 31 PCKHFDVKQIGQAQLPPLYSLVPIFGVGNMLVLLIINCKLCKLTDIYLNLAISDLL 90
Db 28 PCKEGIKAFGEVFLPPLYSLVFVFGLGNSVVLVLFKYKRLSMTDVYLNLAISDLL 87
Qy 91 FLITLPLMAHSAANWVFGNACKLFTGLYHIGYGGIIFILLITDRYLAIVHAFALK 150
Db 88 FVFSLPFWGYAADQWVFGLGKIVSNMVLVGFYSGIFVFLMWSIDRYLAIVHAFSLR 147
Qy 151 ARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVYCGPYPRG---WNNFHTIMRN 207
Db 148 ARTLYGVTSITLSVAVFASVLPGLLSTCYTEHNHTYCKTYSLSNMTTWKVLSSLEIN 207
Qy 208 ILGLVPLLMIVICYSGILTKLLRCNEKKHRAVRVIETIMIVVFLFWTPNYVILLNT 267
Db 208 ILGLVPLGLIMLFCYSMIIRTLQHCCKNEK-NKAVRMIFAVVVLFGFWTPNYVILLFET 266
Qy 268 FQGFFLSNCSTSQLDQATQVETGLMTHCCINPIIYAFVGEKFRS-LFHIALGCR 323
Db 267 LVELEVLDQCTFERYLDVAIQATETLAFVHCCINPIIYFELGKFRKYLQLFKTCR 323

RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S55594
R;Telord, E.A.R.; Watson, M.S.; Aird, H.C.; Petty, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TEL>
A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 40.3%; Score 794.5; DB 2; Length 383;
Best Local Similarity 44.3%; Pred. No. 7.2e-62;
Matches 164; Conservative 60; Mismatches 107; Indels 39; Gaps 7;

Qy 4 TSRSRFRITNNEGSEVTTFFDYD--GAPCHKFDVKQIGQAQLPPLYSLVPIFGVGNM 61
Db 32 TTIASLVPTSNSSDDYDDLDVDESAFCYKSDTTRLAQVVPALYLLVLEFLLGNI 91
Qy 62 LVVLILINCKLCKLTDIYLNLAISDLEFLITLPLMAH--SAANWVFGNACKLFTGL 119
Db 92 LVVIIVIRYMKIKNLTNMLNLNAISDLEFLITLPLFWMHYIGMVDWTFGLSKLLRGV 151
Qy 120 YHIGYGGIIFILLITDRYLAIVHAFALKARTVTFGVVTSVITMLVAVFASVPGIIFT 179
Db 152 CYMSLSYQVFCILLITVDRYLAIVAVYATLRFRTVCGIVTCVTFWLAGLSLPEFFFH 211
Qy 180 KCKEDSVYCGPYFP---RGWNFHTIMRNILGLVPLLMIVICYSGILTKLLRCNE 235
Db 212 GHQDDNGRVQCDPYPEMSTNWRRAHAKVIMLSLILPLLMIVAVCYVIRLLR-RPS 270
Qy 236 KKHRAVRVIETIMIVVFLFWTPNYVILLNTFOEPFLSNCSTSQLDQATQVETGLM 295
Db 271 KKYKAIRLFVIMVAVFVETPTNYVILLSTFHTATLLNLQCALSSNLDWALLITKTVA 330

Query Match 35.8%; Score 704.5; DB 2; Length 354;

Best Local Similarity 47.6%; Pred. No. 5e-54;
Matches 151; Conservative 43; Mismatches 112; Indels 11; Gaps 6;

Qy 24 FDYDYG-PCHKFDVKVIGAGLPPYSLVFIFGVGNMLVLILINCKKLCLTDIYLL 82
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 13 FEYDDSAECYLGDIVAFGFIPLSIFSVLVFTGLVGNLLVLALTNSRKSKITDIYLL 72
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 83 NLAISDLLFLITLPLMAHSAANWVGNAACKLFTGLYHYGYFGGIPFILLTIDRYLAI 142
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 73 NLALSDDLVTATLPFWTHYLIISHEGLHNACKLTAPFFTGPGFGIFITVISIDRYLAI 132
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 143 VHAVFALKARTVTFVVTSVITWLAVFAVPGLIFTCKOKEDSVVVCGPYPRGWNNFH 202
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 133 VLAAANSNNKTVOHVGTISLGWAAAILVASPFMTK-RKONE---CLGDYDEVLOETW 188
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 203 TIMR----NILGLVLPLLIMVICYSGLTKTLRCNEKKHRVVRVIFTIMIYYFLFWTP 258
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 189 PVLRENSENVILGFVPLPILLSPCYCFRIVRTLPSCKNRKA-RAIRLLLLVVVFFLFWTP 247
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 259 YNIVILLNTQEFGLSNCESTSQLDOAQTVTTGLMTHCCINPIIYAFVGEKFRS-LFH 317
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 248 YNIVIFLETLLKYNFPSCGMKRLAWLSVTETVAFSHCCLNPFIYAFAGEKFRYLRH 307
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 318 IALGCRIAPLKQKVCVG 334
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 308 LYNKCLAVALCGRPVHAG 324
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 14

JC4304

Orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to S
A;Reference number: JC4304; MUID:196011651; PMID:7590284
A;Accession: JC4304
A:Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:G665580; PID:AAA91783.1; PID:G665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
C;Genetics:
A;Gene: V28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
P;35-57/Domain: transmembrane #status predicted <TM1>
P;66-88/Domain: transmembrane #status predicted <TM2>
P;104-125/Domain: transmembrane #status predicted <TM3>
P;146-165/Domain: transmembrane #status predicted <TM4>
P;197-217/Domain: transmembrane #status predicted <TM5>
P;230-254/Domain: transmembrane #status predicted <TM6>
P;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 35.4%; Score 698; DB 2; Length 355;
Best Local Similarity 45.3%; Pred. No. 1.9e-53;
Matches 146; Conservative 49; Mismatches 111; Indels 16; Gaps 7;

Qy 18 BEVTFPDY-DYCAPCHKPDVKIQIGALLPPLYSLVFIFGVGNMLVLILINCKKLKCL 76
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 6 ESVTENPEYDDLAEACYIGDIVVFGTVLTSIFYSFALGLVGNLLVLVFNLTNSKKPKSV 65
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 77 TDLYLNLAISDLLFLTLPWAHSAANWVGNAACKLFTGLYHYGYFGGIPFILLTI 136
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 66 TDLYLNLAISDLLFVATLPFWTHYLINEKGLHNACKPTAFFTGPGFGIFITVISI 125
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 137 DRYLAIHVAVFALKARTVTFEGVTSVITWLAVFAVPVGIIFTCKOKEDSVVVCGPYPR 196
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

126 DRYLAIVLAANSMNRTVQHGVTSISLGWAAAILVAAPQFMETK-QKENE---CLGDYPE 181

197 GWNNFHTIMRNI-----LGLVPLLLIMVICYSGILKTLRLCRNEKKRHRVAVRVIITMIVY 252

182 VLQEIPLVLRNVEITNFGFLPLLLIMSYCYFRIIQTLFSCKNHKA-KAIKLILLVVIVF 240

253 PLFWTPYNIIVLLNTFQBFPGLSNCSTESOLDQATQVTTGLGTHCCINPIIYAFVGEKF 312

241 PLFWTPYNIIVMLFETLKLUDFFPPSCDMRKDLRLASVTTETVAFSHCCLNPLIYAFAGEKF 300

313 RS-LFHIALGCRIAPLQKPVCG 333

301 RRYLYHLVGKCLAV-----LCG 317

RESULT 15

JC5942

chemokine receptor - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: JC5942

R:Fan, F.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y. Biochem. Biophys. Res. Commun. 243, 264-268, 1998

A:Title: Cloning and characterization of a novel human chemokine receptor.

A:Reference number: JC5942; MUID:98139902; PMID:9473515

A:Accession: JC5942

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-344 <FAN>

A:Cross-references: UNIPROT:O00421; GB:U97123; NID:G2897070; PID:G2897070; PID:G2897070; PID:AAC39595.1; PID:G2897070

C:Superfamily: vertebrate rhodopsin

Query Match 32.7%; Score 644.5; DB 2; Length 344;

Best Local Similarity 39.9%; Pred. No. 8.7e-49;

Matches 132; Conservative 58; Mismatches 120; Indels 21; Gaps 6;

Qy 27 DYGAPECHKFDVKIQAGLQPLPYSLVIFPGVGNMLVVLILINCKKLKCLTDIYLLNLAI 86

Db 23 DEAEQCDKYDAQALSAQLVPSLSAVFVIGVLDNLVLLVLYKGLKRVENIYLLNLAV 82

Qy 87 SDLLFLTLPLWASAAEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145

Db 83 SNLCFLTLPLFWAHAG-----GDPMKILIGLYFVGLYSETFFNCLLTQRYLVFLHKG 136

Qy 146 VFALKARTVTEGVVTSVITLWLVAFASVPGIIFTRCKQEDSVYVCG-----PYPRG---W 198

Db 137 NFPSARRRVPVCGIITSVLAWTAIALLPEYVYVKPMQEDQYKCAFSRTPLPADSTFW 196

Qy 199 NNFHTIMRNLGLVPLLLIMVICYSGILKTLRLCRNEKKRHRVAVRVIITMIVYFLFWTP 258

Db 197 KHFLTLKMNISVLVPLFIPTFLYVQMRKL---RFREQYSLFLKLVFAIMVYVFLMLWAP 253

Qy 259 YNIVILLNTFQBFPGLSNCSTESOLDQATQVTTGLGTHCCINPIIYAFVGEKFSR--- 314

Db 254 YNIAFFLSTFKHEHSLSDCKSSYNDLKSVDHITKLIATTHCCINPLIYAFLDGTFYSKYLGR 313

Qy 315 LFHIALGCRIAPLQKPVCGPGVPRGNKV 345

Db 314 CFHLRSNTPLPGRGSAOGTSREBPDHSTEV 344

Search completed: June 9, 2005, 16:49:02
Job time : 26.9864 secs

**THIS PAGE LEFT BLANK
BEST AVAILABLE COPY**

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:28:38 ; Search time 115.665 Seconds
(without alignments)
1655.798 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRFRNTNNSGEEV.....GKGKSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 1970 | 100.0 | 374 | 1 CCR2 HUMAN | P41597 homo sapien |
| 2 | 1614.5 | 82.0 | 360 | 1 CCR2 MACMU | O18793 macaca mula |
| 3 | 1346.5 | 68.4 | 373 | 1 CCR2 RAT | O55193 rattus norv |
| 4 | 1332.5 | 67.6 | 373 | 1 CCR2 MOUSE | P51603 mus musculu |
| 5 | 1327.5 | 67.4 | 373 | 1 O6YT42 | O6YT42 sus scrofa |
| 6 | 1252 | 63.6 | 352 | 2 O6WNC2 | O6WNC2 callicebus |
| 7 | 1247 | 63.3 | 354 | 2 O68G28 | O68G28 rattus norv |
| 8 | 1244 | 63.1 | 339 | 2 O9TQ73 | O9TQ73 callithrix |
| 9 | 1244 | 63.1 | 339 | 2 O9TUV8 | O9TUV8 saguinus sp |
| 10 | 1244 | 63.1 | 352 | 2 O6WN98 | O6WN98 callithrix |
| 11 | 1244 | 63.1 | 352 | 2 O9MZA0 | O9MZA0 callithrix |
| 12 | 1244 | 63.1 | 354 | 1 CCR5 MOUSE | P51682 mus musculu |
| 13 | 1243 | 63.1 | 339 | 2 O9TQV5 | O9TQV5 saguinus sp |
| 14 | 1243 | 63.1 | 352 | 2 O95NC4 | O95NC4 ateles geof |
| 15 | 1241 | 63.0 | 352 | 2 O6WNC3 | O6WNC3 leontopithe |
| 16 | 1241 | 63.0 | 352 | 2 O6WN96 | O6WN96 leontopithe |
| 17 | 1241 | 63.0 | 352 | 2 O6WN97 | O6WN97 cebuella py |
| 18 | 1240 | 62.9 | 339 | 2 O9TUV0 | O9TUV0 saguinus sp |
| 19 | 1239 | 62.9 | 352 | 2 O6YT41 | O6YT41 sus scrofa |
| 20 | 1239 | 62.9 | 352 | 2 O9MZ99 | O9MZ99 ateles sp. |
| 21 | 1238.5 | 62.9 | 339 | 2 O9TUV6 | O9TUV6 saguinus sp |
| 22 | 1238 | 62.8 | 339 | 2 O9TUV1 | O9TUV1 saguinus sp |
| 23 | 1237 | 62.8 | 339 | 2 O9TUV9 | O9TUV9 saguinus sp |
| 24 | 1236 | 62.7 | 339 | 2 O9TQW0 | O9TQW0 hylobates c |
| 25 | 1236 | 62.7 | 352 | 1 CCR5_CERTO | O62743 cercocobus |
| 26 | 1236 | 62.7 | 352 | 1 CCR5_HYLLE | O97883 hylobates l |
| 27 | 1236 | 62.7 | 352 | 2 O8HZT9 | O8HZT9 saimiri sci |
| 28 | 1236 | 62.7 | 352 | 2 O6WN92 | O6WN92 leontopithe |
| 29 | 1236 | 62.7 | 352 | 2 O6WN94 | O6WN94 leontopithe |
| 30 | 1236 | 62.7 | 352 | 2 O71R52 | O71R52 cercocobus |
| 31 | 1235 | 62.7 | 339 | 2 O9TGN3 | O9TGN3 macaca fasc |

| | | | | | | |
|----|------|------|-----|---|-----------|--------------------|
| 32 | 1235 | 62.7 | 352 | 2 | O77776 | O77776 cercocobus |
| 33 | 1234 | 62.6 | 339 | 2 | O9TUV5 | O9TUV5 saguinus sp |
| 34 | 1234 | 62.6 | 352 | 2 | O6WN95 | O6WN95 leontopithe |
| 35 | 1233 | 62.6 | 339 | 2 | O9TUV2 | O9TUV2 alouatta ca |
| 36 | 1233 | 62.6 | 352 | 2 | O95NE1 | O95NE1 cercocobus |
| 37 | 1232 | 62.5 | 339 | 2 | O9TUT9 | O9TUT9 macaca mula |
| 38 | 1232 | 62.5 | 339 | 2 | O9TUV0 | O9TUV0 aotus trivi |
| 39 | 1232 | 62.5 | 339 | 2 | O9TUV4 | O9TUV4 callithrix |
| 40 | 1232 | 62.5 | 339 | 2 | O9TUX0 | O9TUX0 hylobates c |
| 41 | 1232 | 62.5 | 352 | 2 | O6WN91 | O6WN91 brachyteles |
| 42 | 1231 | 62.5 | 339 | 2 | O9TUV9 | O9TUV9 hylobates c |
| 43 | 1231 | 62.5 | 352 | 1 | CCR5_HYLM | O95nc0 hylobates m |
| 44 | 1231 | 62.5 | 352 | 2 | O95NC9 | O95nc9 alouatta se |
| 45 | 1231 | 62.5 | 352 | 2 | O9XT12 | O9XT12 cercopithec |

ALIGNMENTS

RESULT 1
ID CCR2 HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CCR-2) (CC-CCR-2) (CCR-2) (CCR2)
GN (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN Name=CCR2; Synonyms=CMKBR2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
chemoattractant protein 1 receptors reveals alternative splicing of
the carboxyl-terminal tails.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
RN [2]
RX MEDLINE=94324942; PubMed=8048929;
RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
chemoattractant protein 1 receptor.";
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [4]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [5]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [6]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [7]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [8]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [9]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [10]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [11]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [12]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [13]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [14]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [15]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [16]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [17]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [18]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [19]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [20]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [21]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [22]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [23]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [24]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [25]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [26]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [27]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [28]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [29]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [30]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [31]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [32]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [33]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [34]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [35]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [36]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [37]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [38]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [39]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [40]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [41]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [42]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [43]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [44]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [45]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [46]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [47]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [48]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [49]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [50]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA Wong L.-M., Myers S.J., Tsou C.-L., Goaling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
chemoattractant protein 1 receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [51]
RX MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;<

Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

[6]
 SULFATION OF TYR-26, AND N-GLYCOSYLATION.
 MEDLINE=20501139; PubMed=11046064;
 RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
 Chakravarty L., Kolatukudy P.E.;
 RA "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
 has tyrosine sulfation in a conserved extracellular N-terminal
 region.";
 RT J. Immunol. 165:5295-5303 (2000).
 CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=A;
 CC IsoId=P41597-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P41597-2; Sequence=VSP_001893;
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@sib.ch).
 CC
 CC EMBL; U03882; AAL19119.1; -
 CC EMBL; U03905; AAL19120.1; -
 CC EMBL; D29984; BAA08253.1; -
 CC EMBL; U80924; AAC51637.1; -
 CC EMBL; U80924; AAC51636.1; -
 CC EMBL; U95626; AAB57791.1; -
 CC EMBL; U95626; AAB57792.1; -
 CC EMBL; AF545480; AAN16400.1; -
 CC PIR; I38450; I38450.
 CC PIR; JC2443; JC2443.
 CC PDB; 1KAD; Model; A=1-349.
 CC PDB; 1KPI; Model; A=1-349.
 CC Genew; HGNC:1603; CCR2.
 CC MIM; 601267; -
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.
 CC GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
 CC GO; GO:0006968; P:cellular defense response; TAS.
 CC GO; GO:0006935; P:chemotaxis; TAS.
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
 CC GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
 CC InterPro; IPR002237; CC 2 receptor.
 CC InterPro; IPR000355; Chkine_receptor.
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSIN.
 CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
 CC 3D-structure; Alternative splicing; G-protein coupled receptor;
 CC Glycoprotein; Polymorphism; Sulfation; Transmembrane.
 CC DOMAIN 1 42
 CC Extracellular (Potential).
 CC TRANSMEM 43 70
 CC 1 (Potential).
 CC DOMAIN 71 80
 CC Cytoplasmic (Potential).
 CC TRANSMEM 81 100
 CC 2 (Potential).
 CC DOMAIN 101 114
 CC Extracellular (Potential).
 CC TRANSMEM 115 136
 CC 3 (Potential).
 CC DOMAIN 137 153
 CC Cytoplasmic (Potential).
 CC TRANSMEM 154 178
 CC 4 (Potential).
 CC DOMAIN 179 206
 CC Extracellular (Potential).
 CC

| FT | TRANSMEM | 207 | 226 | 5 (Potential). |
|----|----------|---------|-----------|--|
| FT | DOMAIN | 227 | 243 | Cytoplasmic (Potential). |
| FT | TRANSMEM | 244 | 268 | 6 (Potential). |
| FT | DOMAIN | 269 | 285 | Extracellular (Potential). |
| FT | TRANSMEM | 286 | 309 | 7 (Potential). |
| FT | DOMAIN | 310 | 374 | Cytoplasmic (Potential). |
| FT | CARBOHYD | 14 | 14 | N-linked (GlcNAc. . .) (Potential). |
| FT | MOD RES | 26 | 26 | Sulfotyrosine. |
| FT | DISULFID | 113 | 190 | By similarity. |
| FT | VARSPLIC | 314 | 374 | SLFHIALGCRIALPQKPCVCGGPGVPRGKGVKVVTOGLLDGR |
| FT | | | | GKGSIGRAPEASLQDKGA -> RYLSVFRKHITKRCK |
| FT | | | | QCPVFRVETVDGVTSTNPTSGEQVSAGL (in |
| FT | | | | isoform B). |
| FT | VARIANT | 64 | 64 | /FTId=VSP_001893. |
| FT | | | | V->I (in dBSNP:1799864). |
| FT | VARIANT | 355 | 355 | /FTId=VAR_014339. |
| FT | | | | G->E. |
| FT | VARIANT | | | /FTId=VAR_014340. |
| FT | | | | F865E0D39E74CF0F CRC64; |
| SQ | SEQUENCE | 374 AA; | 41914 MW; | |

Query Match 100.0%; Score 1970; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1e-118;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| QY | 1 | MLSTSRPIRNTN | SGEEVTF | FDYDYGAPCHKFDVKQIGALPLPLSLVIFGFGVGN | 60 |
|----|-----|--|------------------|--------------------------------------|-----|
| QY | 1 | MLSTSRPIRNTN <td>SGEEVTF</td> <td>FDYDYGAPCHKFDVKQIGALPLPLSLVIFGFGVGN</td> <td>60</td> | SGEEVTF | FDYDYGAPCHKFDVKQIGALPLPLSLVIFGFGVGN | 60 |
| QY | 61 | MLVVLILINCKL | KCLTDIYLLNLAISDL | FLITLPLWAHSAANWVFGNAMCKLFTGLY | 120 |
| QY | 61 | MLVVLILINCKL | KCLTDIYLLNLAISDL | FLITLPLWAHSAANWVFGNAMCKLFTGLY | 120 |
| QY | 121 | HIGYRGIPILL | TDRLYLAIHVA | FALKKARTVTVGVTSTLWVAVFASVPGIIFTK | 180 |
| QY | 121 | HIGYRGIPILL | TDRLYLAIHVA | FALKKARTVTVGVTSTLWVAVFASVPGIIFTK | 180 |
| QY | 181 | CQKEDSVYVCGP | YFPRGWNFNH | IMENILGLVPLLMIVICYSGLKTLRLCRNEKRRH | 240 |
| QY | 181 | CQKEDSVYVCGP | YFPRGWNFNH | IMENILGLVPLLMIVICYSGLKTLRLCRNEKRRH | 240 |
| QY | 241 | AVRVFTIMIVY | FLFWTPYNNIVILLNT | FOEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| QY | 241 | AVRVFTIMIVY | FLFWTPYNNIVILLNT | FOEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| QY | 301 | NPIIYAPVGEK | PSLHIALGCR | IALPQKPCVCGGPGVPRGKGVKVVTOGLLDGRGKSI | 360 |
| QY | 301 | NPIIYAPVGEK | PSLHIALGCR | IALPQKPCVCGGPGVPRGKGVKVVTOGLLDGRGKSI | 360 |
| QY | 361 | GRAPEASLQDKGA | 374 | | |
| QY | 361 | GRAPEASLQDKGA | 374 | | |
| QY | 361 | GRAPEASLQDKGA | 374 | | |
| QY | 361 | GRAPEASLQDKGA | 374 | | |

RESULT 2
 CCR2_MACMU STANDARD; PRT; 360 AA.
 ID CCR2_MACMU
 AC 018793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN Name=CCR2; Synonyms=CMKBR2;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/089922201750290104;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RA "Identification and comparison of eleven rhesus macaque chemokine

RT receptors. ";
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF013958; AAD11572.1; -
 DR InterPro; IPR002237; CC 2 receptor.
 DR InterPro; IPR000355; Cmkine_receptor.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Sulfation; Transmembrane.
 FT DOMAIN 1 42 Extracellular (Potential).
 FT TRANSMEM 43 70 1 (Potential).
 FT DOMAIN 71 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 100 2 (Potential).
 FT DOMAIN 101 114 Extracellular (Potential).
 FT TRANSMEM 115 136 3 (Potential).
 FT DOMAIN 137 153 Cytoplasmic (Potential).
 FT TRANSMEM 154 178 4 (Potential).
 FT DOMAIN 179 206 Extracellular (Potential).
 FT TRANSMEM 207 226 5 (Potential).
 FT DOMAIN 227 243 Cytoplasmic (Potential).
 FT TRANSMEM 244 268 6 (Potential).
 FT DOMAIN 269 285 Extracellular (Potential).
 FT TRANSMEM 286 309 7 (Potential).
 FT DOMAIN 310 360 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc...)(Potential).
 FT MOD_RES 26 26 Sulfotyrosine (By similarity).
 FT DISULFID 113 190 By similarity.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCB913FE9F CRC64;
 Query Match 82.0%; Score 1614.5; DB 1; Length 360;
 Best Local Similarity 96.6%; Pred. No. 6.1e-96;
 Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;
 QY 1 MLSTSRFRINTNTESGEVEVTFDDYDGAPCHKFDVKQIGALLPPLSLVFIFFGVGN 60
 DB 1 MLSTSRFRINTNTESGEVEVTFDDYDGAPCHKFDVKQIGALLPPLSLVFIFFGVGN 60
 QY 61 MLVLLILINCKKLCITDIYLLNLAISDLPLITPLWAHSAANEVFGNAMCKLFTGLY 120
 DB 61 MLVLLILINCKKLCITDIYLLNLAISDLPLITPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGIIPFILLITIDRYLAIVHAVFALKARTTFTGVTSTIWLVAVAVSGIIFTK 180
 DB 121 HIGYFGIIPFILLITIDRYLAIVHAVFALKARTTFTGVTSTIWLVAVAVSGIIFTK 180
 QY 181 CQKEDSVVCPYPPFGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKRRH 240
 DB 181 CQKEDSVVCPYPPFGNNPHITMRNLGLVPLLMVICYSGILKTLRCRNEKRRH 240
 QY 241 AVRVIPTIMIVYFLFWTPYNYIVILLNTFQBEFGLSNCESTSLDQATQVTTGLMTHCCI 300

Db 241 AVRVIPTIMIVYFLFWTPYNYIVILLNTFQBEFGLSNCESTSLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFR---SLF 316
 Db 301 NPIIYAFVGEKFRYLSMP 319
 RESULT 3
 CKR2 RAT
 ID CKR2 RAT STANDARD; PRT; 373 AA.
 AC O55193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 GN C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
 DN Name=Ccr2; Synonyms=Cmkbr2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:11-12(1998).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
 CC chemokines. Transduces a signal by increasing the intracellular
 CC calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
 CC macrophages.
 CC -!- INDUCTION: In animals in which experimental allergic
 CC encephalomyelitis (EAE) has been induced.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U77349; AAC03242.1; -
 DR RGD; 620876; Ccr2.
 DR InterPro; IPR002237; CC 2 receptor.
 DR InterPro; IPR000355; Cmkine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 Extracellular (Potential).
 FT TRANSMEM 61 81 Potential.
 FT DOMAIN 82 91 Cytoplasmic (Potential).
 FT TRANSMEM 92 112 Potential.
 FT DOMAIN 113 128 Extracellular (Potential).
 FT TRANSMEM 129 149 Potential.
 FT DOMAIN 150 170 Cytoplasmic (Potential).
 FT TRANSMEM 171 191 Potential.
 FT DOMAIN 192 220 Extracellular (Potential).
 FT TRANSMEM 221 241 Potential.
 FT DOMAIN 242 256 Cytoplasmic (Potential).
 FT TRANSMEM 257 277 Potential.
 FT DOMAIN 278 301 Extracellular (Potential).
 FT TRANSMEM 302 322 Potential.
 FT DOMAIN 323 373 Cytoplasmic (Potential).

FT DISULFID 126 203 By similarity.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7B8012F5D6FD09 CRC64;
 Query Match 68.4%; Score 1346.5; DB 1; Length 373;
 Best Local Similarity 76.9%; Pred. No. 9.5e-79;
 Matches 257; Conservative 25; Mismatches 45; Indels 7; Gaps 3;
 QY 1 MLSTSRFRTRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOALLPPLYSLVFIQFVGN 60
 DB 14 ILTSHSLFRSQTQELDEGATTPYDDGEPCHKTSVKQIGAWLLPPLYSLVFIQFVGN 73
 QY 61 MLVVLILNCKKLCLETDIYLLNLAISSDLFLTLPLWAHSAANWVFGNCKLFTGLY 120
 DB 74 MLVILILNCKKLCLETDIYLLNLAISSDLFLTLPLWAHSAANWVFGNCKLFTGLY 133
 QY 121 HIGYFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
 DB 134 HIGYFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 193
 QY 181 COXEDSVYVCGPYFPRGWNFNHTIMRNILGLVPLLMVICSYGLKTLALCRNEKKRHR 240
 DB 194 SEQEDDOHTCGPFTPTWKNFQTIMRNILSLIPLLVWVICSYGLKTLALCRNEKKRHR 253
 QY 241 AVRVFTIMVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTETLGMTHCCI 300
 DB 254 AVRLFAIMVYFLFWTPYNNIVLLFTTFQBFGLSNCESTSQLDQATQVTTETLGMTHCCI 313
 QY 301 NPIIYAFVGGKFR---SLF---HIALG-CRIAPL 327
 DB 314 NPIIYAFVGGKFRYLSIFPRKHIKNLCKQCPV 347

RESULT 4

CKR2_MOUSE STANDARD; PRT; 373 AA.
 AC PS1683; Q61172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
 GN (JE/FIC receptor) (MCP-1 receptor).
 GE Name=Ccr2; Synonyms=Cmkbr2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
 RX Boring L., Gosling J., Montecarlo F.S., Luis A.J., Tsou C.-L.,
 RA Charo I.F.,
 RT "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9."
 RT J. Biol. Chem. 271.7551-7558 (1996).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALB/c;
 RX MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;
 RA Kurihara T., Bravo R.;
 RT "Cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC."
 RT J. Biol. Chem. 271.11603-11606 (1996).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97026720; PubMed=8872898;
 RX DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H;
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
 RA Post T.W., Gerard C., Dorf M.E.;
 RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor."
 RT

J. Neurosci. Res. 45:382-391 (1996).
 RL -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5 chemokines. Transduces a signal by increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; U47035; AAC52453.1; -;
 DR EMBL; U51717; AAC52557.1; -;
 DR EMBL; U56819; AAC52784.1; -;
 DR MGD; MGI:106185; Ccr2
 DR GO; GO:0016493; Fc-C chemokine receptor activity; IDA.
 DR GO; GO:0019955; Fc cytokine binding; IPL.
 DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
 DR GO; GO:0030097; P:hemoipoiesis; IMP.
 DR GO; GO:0006959; P:humoral immune response; IMP.
 DR GO; GO:0006954; P:inflammatory response; IMP.
 DR GO; GO:0019233; P:perception of pain; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR002237; CC_2 receptor.
 DR InterPro; IPR000355; Chk kinase receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 55 Extracellular (Potential).
 FT TRANSMEM 56 83 1 (Potential).
 FT DOMAIN 84 93 Cytoplasmic (Potential).
 FT TRANSMEM 94 114 2 (Potential).
 FT DOMAIN 115 127 Extracellular (Potential).
 FT TRANSMEM 128 149 3 (Potential).
 FT DOMAIN 150 166 Cytoplasmic (Potential).
 FT TRANSMEM 167 191 4 (Potential).
 FT DOMAIN 192 219 Extracellular (Potential).
 FT TRANSMEM 220 239 5 (Potential).
 FT DOMAIN 240 256 Cytoplasmic (Potential).
 FT TRANSMEM 257 281 6 (Potential).
 FT DOMAIN 282 298 Extracellular (Potential).
 FT TRANSMEM 299 322 7 (Potential).
 FT DOMAIN 323 373 Cytoplasmic (Potential).
 FT DISULFID 126 203 By similarity.
 FT CONFLICT 39 Y -> H (in Ref. 1).
 FT CONFLICT 184 A -> G (in Ref. 1).
 FT CONFLICT 264 V -> G (in Ref. 1).
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
 Query Match 67.6%; Score 1332.5; DB 1; Length 373;
 Best Local Similarity 76.3%; Pred. No. 7.5e-78;
 Matches 255; Conservative 26; Mismatches 46; Indels 7; Gaps 3;
 QY 1 MLSTSRFRTRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOALLPPLYSLVFIQFVGN 60
 DB 14 ILTSHSLFRSQTQELDEGATTPYDDGEPCHKTSVKQIGAWLLPPLYSLVFIQFVGN 73
 QY 61 MLVVLILNCKKLCLETDIYLLNLAISSDLFLTLPLWAHSAANWVFGNCKLFTGLY 120
 DB 74 MLVILILNCKKLCLETDIYLLNLAISSDLFLTLPLWAHSAANWVFGNCKLFTGLY 133
 QY 121 HIGYFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
 DB 134 HIGYFGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 193


```

QY 196 RG-----WNNFHTMRNLGLVPLLMIVCYSGILKTLRCNEKKHRAVRVIFTIMIV 251
DB 184 FGQYRFWNLETLKMWILGLVPLLVNVCYSGILKTLRCNEKKHRAVRVIFTIMIV 243
QY 252 YFLFWTPYNNIVLLNTQBFGLSNCESTSQLDAQVOTVTLGTHCCINPIIYAFVGEK 311
DB 244 YFLFWPYNIVLLNTQBFGLSNCESSNRLDQAMQVOTVTLGTHCCVNPPIIYAFVGEK 303
QY 312 FRSLSF-----HTA 319
DB 304 FRNYLLVFFOKHIA 317

RESULT 7
Q68G28 ID Q68G28 PRELIMINARY; PRT; 354 AA.
AC Q68G28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Chemokine (C-C) receptor 5.
GN Names=Ckbr5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Haie F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Basak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalls D.Z., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC078756; AAH78756.1; -.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkin receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS02662; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 354 AA; 41081 MW; 4CCBA9AC4EE985C CRC64;
Query Match 63.3%; Score 1247; DB 2; Length 354;
Best Local Similarity 75.6%; Pred. No. 2.2e-72;

```

```

Matches 233; Conservative 29; Mismatches 40; Indels 6; Gaps 2;
QY 17 GEEVTFEFDDY--GAPCHKFQVKQIQAQLPLPLYSIVFIFGFGNMLVVLILINCKK 74
DB 5 GSPTIYDIDYSMSAPCKQFNKQIAAQLPLPLYSIVFIFGFGNMLVVLILINCKK 64
QY 75 CLTDIYLLMLAISDLLFLTLPLWAHSAANEWVFGNAMCKLFTGLXHYGFGGIFILL 134
DB 65 SMTDIYLFNLAISDLLFLTLPLWAHSAANEWVFGNAMCKLFTGLXHYGFGGIFILL 124
QY 135 TIDRYLAIHVAHPALKARTVTFGVTSVITWLVAVFASVPGIIFTCKQKEDSVVCGPYF 194
DB 125 TIDRYLAIHVAHPALKARTVTFGVTSVITWLVAVFASVPGIIFTCKQKEDSVVCGPYF 184
QY 195 P-----RGWNNFHTMRNLGLVPLLMIVCYSGILKTLRCNEKKHRAVRVIFTIMI 250
DB 185 PRIQYRFWKHFQTLKMWILGLVPLLVNVCYSGILKTLRCNEKKHRAVRVIFTIMI 244
QY 251 VYFLFWTPYNNIVLLNTQBFGLSNCESTSQLDAQVOTVTLGTHCCINPIIYAFVGE 310
DB 245 VYFLFWTPYNNIVLLNTQBFGLSNCESSNRLDQAMQVOTVTLGTHCCINPIIYAFVGE 304
QY 311 KFRSLFHI 318
DB 305 KFRNYLSV 312

RESULT 8
Q9TQT3 ID Q9TQT3 PRELIMINARY; PRT; 339 AA.
AC Q9TQT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN Names=CCRS;
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=22942991; PubMed=14581567;
RX DOI=10.1128/JVI.77.22.12310-12318.2003;
RA Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA Kunstman J., Stanton J., Agly M., Shibata R., Yoder A.D., Pillai S.,
RA Doms R.W., Marx P., Wolinsky S.M.;
RA "Structure and function of CC-chemokine receptor 5 homologues derived
RT from representative primate species and subspecies of the taxonomic
RT suborders Prosimii and Anthropoidea."
J. Virol. 77:12310-12318(2003).
[2]
SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF162021; AAD47776.1; -.
DR EMBL; AF161934; AAD47691.1; -.
DR EMBL; AF161935; AAD47692.1; -.
DR EMBL; AF161936; AAD47693.1; -.
DR EMBL; AF161937; AAD47694.1; -.
DR EMBL; AF161938; AAD47695.1; -.
DR EMBL; AF161939; AAD47696.1; -.
DR EMBL; AF161940; AAD47697.1; -.
DR EMBL; AF161944; AAD47700.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00923; BlueCu_1.

```


CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY278745; AAQ20013.1; -.
 DR EMBL; AY278744; AAQ20012.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC 5 receptor.
 DR InterPro; IPR000355; ChemKine_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40522 MW; PF0D0A852E553AF5 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3.4e-72;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFTFGVGNMLVLLINCKLKLTIDYL 81
 DB 10 YDIDYGPSEPCRKIDVKQGAHLLPPLYSVMVFLFGVGNMLVLLINCKLKLSMTDYL 69

QY 82 LNLAIISDLLFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGIFILLTIDRYLA 141
 DB 70 LNLAIISDLIFLFTVPFWAHYAAGWDGNTWCQFLTGLYIFGFSGIFILLTIDRYLA 129

QY 142 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 DB 130 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVVCGPYFP 189

QY 198 WNNFHTIMRNILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWT 257
 DB 190 WKNPFELKWLGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWA 249

QY 258 PYNIVILLNTFOBPFGLNSCESTSLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLF- 316
 DB 250 PYNIVILLNTYQEFGLNCCSSNRLDQAMQVTTGLMTHCCNPIIYAFVGEKFRNYLA 309

QY 317 -----HIA 319
 DB 310 VFFQKHIA 317

RESULT 11
 Q9MZA0 PRELIMINARY; PRT; 352 AA.
 AC Q9MZA0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CC chemokine receptor 5 (Chemokine receptor CCR5).
 GN Names=CCR5; Synonyms=ccr5;
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20317091; PubMed=10747879; DOI=10.1074/jbc.M000169200;
 RA Mummidi S., Bameshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
 RA Begum K., Galvis M.C., Kosteki V., Valente A.J., Murthy K.K.,
 RA Haro L., Dolan J.S., Allan J.S., Ahuja S.K.;
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
 and mRNA. Potential roles for haplotype and mRNA diversity,

RT differential haplotype-specific transcriptional activity, and altered
 RT transcription factor binding to polymorphic nucleotides in the
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.;
 RL J. Biol. Chem. 275:18946-18961(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22174698; PubMed=12186836;
 RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
 RT "Blockade of HIV-1 infection of New World monkey cells occurs
 RT primarily at the stage of virus entry";
 RL J. Exp. Med. 196:431-445(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
 RA Seanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF252554; AAF87984.1; -.
 DR EMBL; AF452614; AAN14530.1; -.
 DR EMBL; AY278743; AAQ20011.1; -.
 DR EMBL; AF177878; AAK43361.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR002240; CC 5 receptor.
 DR InterPro; IPR000355; ChemKine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40465 MW; PF0D0A8D06F7B8F5 CRC64;

Query Match 63.1%; Score 1244; DB 2; Length 352;
 Best Local Similarity 76.6%; Pred. No. 3.4e-72;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFTFGVGNMLVLLINCKLKLTIDYL 81
 DB 10 YDIDYGPSEPCRKIDVKQGAHLLPPLYSVMVFLFGVGNMLVLLINCKLKLSMTDYL 69

QY 82 LNLAIISDLLFLITLPLWAHSAANEVFGNAMCKLTGLYHIGYFGGIFILLTIDRYLA 141
 DB 70 LNLAIISDLIFLFTVPFWAHYAAGWDGNTWCQFLTGLYIFGFSGIFILLTIDRYLA 129

QY 142 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 DB 130 IVHAVFALKARTVTFGVVTSVITMLVAVFASVPGIIFTKCKEDSVVCGPYFP 189

QY 198 WNNFHTIMRNILGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWT 257
 DB 190 WKNPFELKWLGLVPLLMVTCYSGILKTLRCNEKRRHRAVRVIFIMIVYFLFWA 249

QY 258 PYNIVILLNTFOBPFGLNSCESTSLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLF- 316
 DB 250 PYNIVILLNTYQEFGLNCCSSNRLDQAMQVTTGLMTHCCNPIIYAFVGEKFRNYLA 309

QY 317 -----HIA 319
 DB 310 VFFQKHIA 317

RESULT 12

| CC | CKR5_MOUSE | STANDARD; | PRT; | 354 AA. |
|----|---|-----------------------------------|-----------------|---------|
| ID | CKR5_MOUSE | STANDARD; | PRT; | 354 AA. |
| AC | P51682; O35313; | O35891; P97308; | P97405; Q61867; | |
| DT | 01-OCT-1996 | (Rel. 34, Created) | | |
| DT | 15-JUL-1998 | (Rel. 36, Last sequence update) | | |
| DT | 25-OCT-2004 | (Rel. 45, Last annotation update) | | |
| DE | C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1 alpha receptor). | | | |
| DE | Name=CKr5; Synonyms=Cmkbr5; | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=129/SvJ; TISSUE=Spleen; | | | |
| RX | MEDLINE=96205938; PubMed=86311787; DOI=10.1074/jbc.271.13.7551; | | | |
| RA | Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L., Charo I.F.; | | | |
| RA | "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9."; | | | |
| RT | J. Biol. Chem. 271:7551-7558(1996). | | | |
| RN | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6 X CBA; TISSUE=Thymus; | | | |
| RC | MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445; | | | |
| RX | Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.; | | | |
| RA | "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor."; | | | |
| RT | J. Biol. Chem. 271:14445-14451(1996). | | | |
| RN | [3] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=129/Ola; | | | |
| RC | Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.; | | | |
| RA | Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases. | | | |
| RA | [4] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; | | | |
| RC | MEDLINE=98001387; PubMed=9343222; | | | |
| RA | Kuhmann S.B., Platt E.J., Kozak S.L., Kabat D.; | | | |
| RX | "Polymorphisms in the CKR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."; | | | |
| RT | J. Virol. 71:8642-8656(1997). | | | |
| RN | [5] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=129; | | | |
| RC | MEDLINE=97404635; PubMed=92611347; | | | |
| RX | Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H., Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.; | | | |
| RA | "Two distinct CKR5 domains can mediate coreceptor usage by human immunodeficiency virus type 1."; | | | |
| RT | J. Virol. 71:6305-6314(1997). | | | |
| RN | [6] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RC | Guo B., Kuno K., Harada A., Matsushima K.; | | | |
| RA | Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases. | | | |
| RL | -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. | | | |
| CC | -I- SUBCELLULAR LOCATION: Integral membrane protein. | | | |
| CC | -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines. | | | |
| CC | -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way | | | |

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to licensee@isb-sib.ch).

| CC | EMBL; U47036; AAC52454.1; -- | DR | EMBL; X94151; CAAG3867.1; -- | DR | EMBL; U85855; AAB37273.1; -- | DR | EMBL; U83327; AAC53386.1; -- | DR | EMBL; AF022990; AAC53389.1; -- | DR | EMBL; AF019772; AAB71183.1; -- | DR | EMBL; D83648; BAA12024.1; -- | DR | MGD; MG1:107182; Ccr5. | DR | GO; GO:0016493; P:C-C chemokine receptor activity; IDA. | DR | GO; GO:0006952; P:defense response; IMP. | DR | InterPro; IPR002240; CC 5_receptor. | DR | InterPro; IPR00355; Chkline_receptor. | DR | InterPro; IPR00276; GPCR_Rhodopsn. | DR | Pfam; PF00001; 7tm1.1; 1. | DR | PRINTS; PR00237; GPCRRHODOPSN. | DR | PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. | DR | PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1. | DR | G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane. | KW | DOMAIN 1 32 | FT | EXTRACELLULAR (Potential). | FT | TRANSMEM 33 60 | FT | DOMAIN 61 70 | FT | TRANSMEM 71 91 | FT | DOMAIN 92 104 | FT | TRANSMEM 105 126 | FT | DOMAIN 127 143 | FT | TRANSMEM 144 168 | FT | DOMAIN 169 200 | FT | TRANSMEM 201 220 | FT | DOMAIN 221 237 | FT | TRANSMEM 238 262 | FT | DOMAIN 263 279 | FT | TRANSMEM 280 303 | FT | DOMAIN 304 354 | FT | DISULFID 103 180 | FT | CARBOHYD 270 270 | FT | VARIANT 11 11 | FT | VARIANT 62 62 | FT | VARIANT 66 66 | FT | VARIANT 97 97 | FT | VARIANT 109 109 | FT | VARIANT 156 156 | FT | VARIANT 160 160 | FT | VARIANT 185 185 | FT | VARIANT 213 213 | FT | VARIANT 318 318 | FT | VARIANT 337 337 | FT | CONFLICT 3 3 | FT | CONFLICT 80 80 | FT | CONFLICT 145 145 | FT | CONFLICT 190 190 | FT | CONFLICT 208 208 | FT | CONFLICT 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64; | SQ | SEQUENCE | Query Match | Best Local Similarity | Matches | Conservative | Score | DB 1; Length | 354; | 63.1%; | 75.3%; | 232; | 29; | 2; | Indels | 6; | Gaps | 2; | 17 | GEEVTFPFDDYDG--APCHKFDVKIQGAQLLPPLYSLVFFGFGVGNMLVVLLINCKKLK | 74 | 5 | GSVPPTYVIDDYGMASPCQKINKVAQIAQLLPPLYSLVFFGFGVGNMWVLISCKKLK | 64 | 75 |
|----|------------------------------|----|------------------------------|----|------------------------------|----|------------------------------|----|--------------------------------|----|--------------------------------|----|------------------------------|----|------------------------|----|---|----|--|----|-------------------------------------|----|---------------------------------------|----|------------------------------------|----|---------------------------|----|--------------------------------|----|--|----|--|----|--|----|-------------|----|----------------------------|----|----------------|----|--------------|----|----------------|----|---------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|------------------|----|---------------|----|---------------|----|---------------|----|---------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|--------------|----|----------------|----|------------------|----|------------------|----|------------------|----|--|----|----------|-------------|-----------------------|---------|--------------|-------|--------------|------|--------|--------|------|-----|----|--------|----|------|----|----|---|----|---|---|----|----|
|----|------------------------------|----|------------------------------|----|------------------------------|----|------------------------------|----|--------------------------------|----|--------------------------------|----|------------------------------|----|------------------------|----|---|----|--|----|-------------------------------------|----|---------------------------------------|----|------------------------------------|----|---------------------------|----|--------------------------------|----|--|----|--|----|--|----|-------------|----|----------------------------|----|----------------|----|--------------|----|----------------|----|---------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|----------------|----|------------------|----|------------------|----|---------------|----|---------------|----|---------------|----|---------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|-----------------|----|--------------|----|----------------|----|------------------|----|------------------|----|------------------|----|--|----|----------|-------------|-----------------------|---------|--------------|-------|--------------|------|--------|--------|------|-----|----|--------|----|------|----|----|---|----|---|---|----|----|

| | | | |
|--|--|--|-----|
| QY | 24 | FDYDYG--APCHKFDVKQIGAGQALLPPLYSLSLVFIIFGFVGNMLVLLINCKKLKCLTDIYVL | 81 |
| DB | 3 | YDIDYGESEPCRKIDVKQGAHLLPPLYSVMVFLFGFVGNMLVLLINCKPKGMSMTDIYVL | 62 |
| QY | 82 | LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLXHYIGYFGGIFFIILLTIDRYLA | 141 |
| DB | 63 | LNLAISDLIIFLFTVFWAHYAAGWDGNTWCQFLTGLYIFGFSGIFFIILLTIDRYLA | 122 |
| QY | 142 | IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIIFTKQKEDSVYVCGPYFPRG---- | 197 |
| DB | 123 | IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSKQGVHYTCSPHYFPGQYQF | 182 |
| QY | 198 | WNPHITMIRNMLGLVLPDLLIMVICYSIGILKTLICRNEKKHRAVRVIFTTIMIVYFLEWTF | 257 |
| DB | 183 | WKNFETLKWIVLGLVLPDLLIMVICYSIGILKTLICRNEKKHRAVRVIFTTIMIVYFLEWA | 242 |
| QY | 258 | PYNIIVLLNTQFQFFGLSNCESTSQLDAQTVTETLGTWTHCCINPIIYAFVGEKFRSLF- | 316 |
| DB | 243 | PYNIIVLLNTQFQFFGLSNCSNRLRDLQAVTETLGTWTHCCVNPPIIYAFVGEKFRNLYV | 302 |
| QY | 317 | -----HIA 319 | |
| DB | 303 | VFFQKHIA 310 | |
| RESULT 14 | | | |
| Q95NC4 PRELIMINARY; PRT; 352 AA. | | | |
| AC | Q95NC4 | | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Created) | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Last sequence update) | |
| DT | 01-MAR-2004 | (TrEMBLrel. 26, Last annotation update) | |
| DE | C-C chemokine receptor 5. | | |
| GN | Name=CCRS; | | |
| OS | Ateles geoffroyi (Black-handed spider monkey). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles; | | |
| OX | NCBI_TaxID=9509; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Zhang Y., Ryder O.A., Zhang Y., | | |
| RL | Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity). | | |
| CC | -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. | | |
| DR | EMBL; AF177885; AAK43368.1; - | | |
| DR | GO; GO:0016021; C:integral to membrane; IEA. | | |
| DR | GO; GO:0016493; P:C-C chemokine receptor activity; IEA. | | |
| DR | GO; GO:0004872; F:receptor activity; IEA. | | |
| DR | GO; GO:0001584; F:rhodopsin-like receptor activity; IEA. | | |
| DR | GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA. | | |
| DR | InterPro; IPR000923; BlueCu 1. | | |
| DR | InterPro; IPR002240; CC 5 receptor. | | |
| DR | InterPro; IPR000355; Chkline_receptor. | | |
| DR | InterPro; IPR000276; GPCR_Rhodpsn. | | |
| DR | Pfam; PF00001; 7tm1_1. | | |
| DR | PRINTS; PR00657; CCHEMOKINER. | | |
| DR | PRINTS; PR01110; CHEMOKINERS. | | |
| DR | PRINTS; PR00237; GPCRHDOPSN. | | |
| DR | PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1. | | |
| DR | PROSITE; PS00237; G PROTEIN RECP FL 1; 1. | | |
| DR | PROSITE; PSS0262; G PROTEIN RECP FL 2; 1. | | |
| KW | G-protein coupled receptor; Receptor; Transmembrane. | | |
| SQ | SEQUENCE 352 AA; 40440 MW; POA686CB4FE3964B CRC64; | | |
| Query Match 63.1%; Score 1243; DB 2; Length 352; | | | |
| Best Local Similarity 76.6%; Pred. No. 4e-72; | | | |
| Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3 | | | |
| QY | 24 | FDYDYG--PCHKFDVKQIGAGQALLPPLYSLSLVFIIFGFVGNMLVLLINCKKLKCLTDIYVL | 81 |
| DB | 10 | YDIDYGESEPCRKIDVKQGAHLLPPLYSVMVFLFGFVGNMLVLLINCKPKGMSMTDIYVL | 69 |
| QY | 82 | LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLXHYIGYFGGIFFIILLTIDRYLA | 141 |

```
Db 70 LNLAISSLFLFTVFFWAHVAAGQMDFGNTMCQFLTGLYFGPSGIFFIILLTIDRYLA 129
Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFPRG---- 197
Db 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFPRG---- 189
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 257
Db 190 WKNFETLWILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWA 249
Qy 258 PYNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLF- 316
Db 250 PYNIVLLNTYQEFFGLNCCSSNRLDQAMQVTTGLMTHCCVNPPIIYAFVGEKFRNLL 309
Qy 317 -----HIA 319
Db 310 VFFQKHIA 317

RESULT 15
Q6WN93
ID Q6WN93 PRELIMINARY; PRT; 352 AA.
AC Q6WN93;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CC chemokine receptor 5.
GN Name=ccr5;
OS Leontopithecus chrysopygus (Gold-and-black lion tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Leontopithecus.
OX NCBI_TaxID=58710;
RN [1]
RP SEQUENCE FROM N.A.
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA Seanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY278750; AAQ20018.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000923; BlueCh1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40437 MW; SEC1864238503783 CRC64;

Query Match 63.0%; Score 1241; DB 2; Length 352;
Best Local Similarity 76.3%; Pred. No. 5.3e-72;
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

Qy 24 FDYDGA--PCHKFDVQIGAGQLLPPLYSLSVTFPGVGNMLVVLINCKLCLTDIYL 81
Db 10 YDIDYGASBPCRKIDVQMGAGHLLPPLYSVMVFLFGVGNMLVVLINCKRPSMTDIYL 69
Qy 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
Db 70 LNLAISSLFLFTVFFWAHVAAGQMDFGNTMCQFLTGLYFGPSGIFFIILLTIDRYLA 129
```

```
Qy 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFPRG---- 197
Db 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFPRG---- 189
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 257
Db 190 WKNFETLWILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWA 249
Qy 258 PYNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLF- 316
Db 250 PYNIVLLNTYQEFFGLNCCSSNRLDQAMQVTTGLMTHCCVNPPIIYAFVGEKFRNLL 309
Qy 317 -----HIA 319
Db 310 VFFQKHIA 317
```

Search completed: June 9, 2005, 16:48:06
Job time : 117.165 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:37:43 ; Search time 31.0817 Seconds
(without alignments)
898.236 Million cell updates/sec

Title: US-10-791-166-2

Perfect score: 1970

Sequence: 1 MLSTSRFRIRNTNESGEV.....GKSGSIGRAPEASLDQKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 1970 | 100.0 | 374 | 1 | US-08-450-393A-2 |
| 2 | 1970 | 100.0 | 374 | 3 | US-08-446-669-2 |
| 3 | 1970 | 100.0 | 374 | 4 | US-10-039-659A-14 |
| 4 | 1970 | 100.0 | 374 | 4 | US-09-625-573-2 |
| 5 | 1970 | 100.0 | 374 | 5 | PCT-US95-00476-2 |
| 6 | 1970 | 100.0 | 387 | 4 | US-09-949-016-11222 |
| 7 | 1823 | 92.5 | 344 | 3 | US-08-466-343D-9 |
| 8 | 1823 | 92.5 | 344 | 4 | US-09-502-783A-9 |
| 9 | 1727.5 | 87.7 | 329 | 4 | US-09-502-783A-9 |
| 10 | 1727.5 | 87.7 | 329 | 4 | US-09-339-912A-9 |
| 11 | 1727.5 | 87.7 | 329 | 4 | US-09-195-662A-9 |
| 12 | 1651.5 | 83.8 | 360 | 1 | US-08-450-393A-4 |
| 13 | 1651.5 | 83.8 | 360 | 3 | US-08-446-669-4 |
| 14 | 1651.5 | 83.8 | 360 | 3 | US-09-045-583-50 |
| 15 | 1651.5 | 83.8 | 360 | 4 | US-09-534-185-50 |
| 16 | 1651.5 | 83.8 | 360 | 4 | US-09-131-827A-2 |
| 17 | 1651.5 | 83.8 | 360 | 4 | US-09-625-573-4 |
| 18 | 1651.5 | 83.8 | 360 | 5 | PCT-US95-00476-4 |
| 19 | 1651.5 | 83.8 | 377 | 4 | US-09-949-016-11221 |
| 20 | 1651.5 | 83.8 | 360 | 4 | US-09-131-827A-20 |
| 21 | 1645.5 | 83.5 | 360 | 4 | US-08-833-752-7 |
| 22 | 1645.5 | 83.5 | 360 | 4 | US-09-938-719-7 |
| 23 | 1645.5 | 83.5 | 360 | 4 | US-09-939-226B-7 |
| 24 | 1645.5 | 83.5 | 360 | 4 | US-09-826-509-473 |
| 25 | 1614.5 | 82.0 | 360 | 3 | US-09-045-583-51 |
| 26 | 1614.5 | 82.0 | 360 | 4 | US-09-534-185-51 |
| 27 | 1589.5 | 80.7 | 347 | 1 | US-08-461-244-3 |

| | | | | | | |
|----|------|------|-----|---|-------------------|-------------------|
| 28 | 1236 | 62.7 | 352 | 3 | US-09-517-605-5 | Sequence 5, Appli |
| 29 | 1234 | 62.6 | 354 | 3 | US-08-724-984A-2 | Sequence 2, Appli |
| 30 | 1230 | 62.4 | 352 | 3 | US-09-045-583-52 | Sequence 52, Appl |
| 31 | 1230 | 62.4 | 352 | 4 | US-09-534-185-52 | Sequence 52, Appl |
| 32 | 1224 | 62.1 | 352 | 3 | US-09-087-232A-13 | Sequence 13, Appl |
| 33 | 1224 | 62.1 | 352 | 3 | US-08-861-105-14 | Sequence 14, Appl |
| 34 | 1224 | 62.1 | 352 | 3 | US-08-575-967A-2 | Sequence 2, Appli |
| 35 | 1224 | 62.1 | 352 | 4 | US-08-833-752-5 | Sequence 5, Appli |
| 36 | 1224 | 62.1 | 352 | 4 | US-09-502-783A-2 | Sequence 2, Appli |
| 37 | 1224 | 62.1 | 352 | 4 | US-09-796-202-1 | Sequence 1, Appli |
| 38 | 1224 | 62.1 | 352 | 4 | US-09-938-719-5 | Sequence 5, Appli |
| 39 | 1224 | 62.1 | 352 | 4 | US-09-502-784A-2 | Sequence 2, Appli |
| 40 | 1224 | 62.1 | 352 | 4 | US-09-339-912A-2 | Sequence 2, Appli |
| 41 | 1224 | 62.1 | 352 | 4 | US-08-771-276-2 | Sequence 2, Appli |
| 42 | 1224 | 62.1 | 352 | 4 | US-08-771-276-20 | Sequence 20, Appl |
| 43 | 1224 | 62.1 | 352 | 4 | US-09-939-226B-5 | Sequence 5, Appli |
| 44 | 1224 | 62.1 | 352 | 4 | US-09-195-662A-2 | Sequence 2, Appli |
| 45 | 1218 | 61.8 | 352 | 4 | US-09-826-509-477 | Sequence 477, App |

ALIGNMENTS

RESULT 1
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/0205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-393A-2

Query Match 100.0%; Score 1970; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFRIRNTNESGEVTTTFDDYDYGAPCHKFDVKQIQAQLLPYLSLVFIQFVGN 60
Db 1 MLSTSRFRIRNTNESGEVTTTFDDYDYGAPCHKFDVKQIQAQLLPYLSLVFIQFVGN 60

QY 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLLMVICYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLLMVICYSGILKTLRCNEKKRHR 240
QY 241 AVRVITIMVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300
DB 241 AVRVITIMVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSKI 360
DB 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSKI 360
QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 2

US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
Query Match 100.0%; Score 1970; DB 3; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGN 60
|||||

DB 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLLMVICYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLLMVICYSGILKTLRCNEKKRHR 240
QY 241 AVRVITIMVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300
DB 241 AVRVITIMVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSKI 360
DB 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKSKI 360
QY 361 GRAPEASLQDKEGA 374
DB 361 GRAPEASLQDKEGA 374

RESULT 3

US-10-039-659A-14
; Sequence 14, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-659A-14
Query Match 100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGN 60
DB 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAIISDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITWLVAVPASVPGIIFTK 180

QY 181 COKEDSVVCGPYPRGNNPHITMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHR 240
 Db 181 COKEDSVVCGPYPRGNNPHITMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFOBFFGLSNCESTSQLDQATQVETLGMTHCCI 300
 Db 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFOBFFGLSNCESTSQLDQATQVETLGMTHCCI 300
 QY 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVPRGNKVVTTQGLLDGRGKSKI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVPRGNKVVTTQGLLDGRGKSKI 360
 QY 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 4
 US-09-625-573-2
 ; Sequence 2, Application US/09625573
 ; Patent No. 6730301
 ; GENERAL INFORMATION:
 ; APPLICANT: Charo, Israel
 ; Coughlin, Shaun
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/625,573
 ; FILING DATE: 25-Jul-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,669
 ; FILING DATE: May 25, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Neeley, Richard
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: UCAL-237/01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5000
 ; TELEFAX: 415-857-0663
 ; TELEX: 380816COOLEYPA
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-625-573-2

Query Match 100.0%; Score 1970; DB 4; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.3e-150;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRPIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSILVFIQFVGN 60
 Db 1 MLSTSRSRPIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSILVFIQFVGN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTTSVITWLVAVFASVFGIIFTK 180
 Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTTSVITWLVAVFASVFGIIFTK 180
 QY 181 COKEDSVVCGPYPRGNNPHITMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHR 240
 Db 181 COKEDSVVCGPYPRGNNPHITMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFOBFFGLSNCESTSQLDQATQVETLGMTHCCI 300
 Db 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFOBFFGLSNCESTSQLDQATQVETLGMTHCCI 300
 QY 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVPRGNKVVTTQGLLDGRGKSKI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVPRGNKVVTTQGLLDGRGKSKI 360
 QY 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 5
 PCT-US95-00476-2
 ; Sequence 2, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-00476-2

Query Match 100.0%; Score 1970; DB 5; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.3e-150;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRPIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSILVFIQFVGN 60
 Db 1 MLSTSRSRPIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIQAQLLPPLYSILVFIQFVGN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKCLTDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPIILLITDYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTK 180
 Db 121 HIGYFGGIFPIILLITDYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTK 180
 QY 181 CQKEDSVVCGPYFPRGNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240
 Db 181 CQKEDSVVCGPYFPRGNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVFTIMVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCI 300
 Db 241 AVRVFTIMVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCI 300
 QY 301 NPIIYAFVGEKPSLFHIALGCRPIAQKPCVCGPVRPGKNNKVVTTQGLLDGRGKSI 360
 Db 301 NPIIYAFVGEKPSLFHIALGCRPIAQKPCVCGPVRPGKNNKVVTTQGLLDGRGKSI 360
 QY 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374

RESULT 6
 US-09-949-016-11222
 ; Sequence 11222, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11222
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-11222

Query Match 100.0%; Score 1970; DB 4; Length 387;
 Best Local Similarity 100.0%; Pred. No. 4.5e-150;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRFRIRNTNESGEVTFPDYDYGAPCHKFDVKQIQAOLLPPLYSLVIFGFGVN 60
 Db 14 MLSTSRFRIRNTNESGEVTFPDYDYGAPCHKFDVKQIQAOLLPPLYSLVIFGFGVN 73
 QY 61 MLVVLILINCKKCLTDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 Db 74 MLVVLILINCKKCLTDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 133
 QY 121 HIGYFGGIFPIILLITDYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTK 180
 Db 134 HIGYFGGIFPIILLITDYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTK 193
 QY 181 CQKEDSVVCGPYFPRGNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 240
 Db 194 CQKEDSVVCGPYFPRGNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHR 253
 QY 241 AVRVFTIMVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCI 300
 Db 254 AVRVFTIMVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCI 313
 QY 301 NPIIYAFVGEKPSLFHIALGCRPIAQKPCVCGPVRPGKNNKVVTTQGLLDGRGKSI 360

Db 314 NPIIYAFVGEKPSLFHIALGCRPIAQKPCVCGPVRPGKNNKVVTTQGLLDGRGKSI 373
 QY 361 GRAPEASLQDKEGA 374
 Db 374 GRAPEASLQDKEGA 387
 RESULT 7
 US-08-466-343D-9
 ; Sequence 9, Application US/08466343D
 ; Patent No. 6025154
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, Yi
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
 ; CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVE., NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,343D
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 344 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-466-343D-9

Query Match 92.5%; Score 1823; DB 3; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.3e-138;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EVVTFPDYDYGAPCHKFDVKQIQAOLLPPLYSLVIFGFGVNMLVLLINCKKCLT 77
 Db 1 EVVTFPDYDYGAPCHKFDVKQIQAOLLPPLYSLVIFGFGVNMLVLLINCKKCLT 60
 QY 78 DIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFPIILLIT 137
 Db 61 DIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFPIILLIT 120
 QY 138 RYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTKCQKEDSVVCGPYFPRG 197
 Db 121 RYLAIHVAHPALKARTVTFGVTSVITLWVAVPASPGLIFTKCQKEDSVVCGPYFPRG 180
 QY 198 WNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHRARVIFTIMIVYFLFWT 257
 Db 181 WNNFHTIMRNILGLVPLLIWVCYSGILKTLRCRNEKKRHRARVIFTIMIVYFLFWT 240
 QY 258 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCINPIIYAFVGEKPSLFH 317
 Db 241 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLTGMTHCCINPIIYAFVGEKPSLFH 300

Qy 318 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 361
 Db 301 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 344

RESULT 8

US-09-502-784A-9
 ; Sequence 9, Application US/09502784A
 ; Patent No. 6743594
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
 ; TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
 ; FILE REFERENCE: 1488.1150005
 ; CURRENT APPLICATION NUMBER: US/09/502,784A
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/195,662
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 08/466,343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn Version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; ORGANISM: Protein

Query Match 92.5%; Score 1823; DB 4; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2.3e-138;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 77
 Db 1 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 60
 Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 137
 Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 120
 Qy 138 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYPPRG 197
 Db 121 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYPPRG 180
 Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLWT 257
 Db 181 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLWT 240
 Qy 258 PYNIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
 Db 241 PYNIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300
 Qy 318 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 361
 Db 301 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 344

RESULT 9

US-09-502-783A-9
 ; Sequence 9, Application US/09502783A
 ; Patent No. 6511826
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven M.
 ; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
 ; TITLE OF INVENTION: HDGNR10
 ; FILE REFERENCE: 1488.1150006
 ; CURRENT APPLICATION NUMBER: US/09/502,783A
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 08/466,343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Protein
 ; ORGANISM: Protein

US-09-502-783A-9
 Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 9.8e-131;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 Qy 18 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 77
 Db 1 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 60
 Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 137
 Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 105
 Qy 138 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYPPRG 197
 Db 106 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYPPRG 165
 Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLWT 257
 Db 166 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRHRAVRVIFTIMIVYFLWT 225
 Qy 258 PYNIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
 Db 226 PYNIVILLNTFOEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 285
 Qy 318 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 361
 Db 286 IALGCRAPLOKPVCGGPGVRPGKRVKVTQTGLDGRGKKSIG 329

RESULT 10

US-09-339-912A-9
 ; Sequence 9, Application US/09339912A
 ; Patent No. 6759519
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
 ; TITLE OF INVENTION: (CCR5 Receptor)
 ; FILE REFERENCE: 1488.1150003
 ; CURRENT APPLICATION NUMBER: US/09/339,912A
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 09/195,662
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 08/466,343
 ; PRIOR FILING DATE: 1995-06-06
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 329
 ; TYPE: PRT
 ; ORGANISM: Protein
 ; ORGANISM: Protein

US-09-339-912A-9
 Query Match 87.7%; Score 1727.5; DB 4; Length 329;
 Best Local Similarity 95.6%; Pred. No. 9.8e-131;
 Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 Qy 18 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 77
 Db 1 EVVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMVLVLLINCKKLKLT 60
 Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 137
 Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTID 105
 Qy 138 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYPPRG 197

Db 106 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPIFPRG 165
Qy 198 WNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHRVAVRVIPTIMIVYFLFWT 257
Db 166 WNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHRVAVRVIPTIMIVYFLFWT 225
Qy 258 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317
Db 226 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 285
Qy 318 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361
Db 286 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 329
RESULT 11
US-09-195-662A-9
; Sequence 9, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-195-662A-9
Query Match 87.7%; Score 1727.5; DB 4; Length 329;
Best Local Similarity 95.6%; Pred. No. 9.8e-131;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
Qy 18 EEVTFDFDYDYGAPCHKFDVKQIGALLPPLYSIVFIFGVGNMVLVILINCKLCKLT 77
Db 1 EEVTFDFDYDYGAPCHKFDVKQIGALLPPLYSIVFIFGVGNMVLVILINCKLCKLT 60
Qy 78 DIVLLNLAISDLLFLITPLWHAHSAANWVFGNAMCKLFTGLYHIGVFGGIFPIILLTID 137
Db 61 DIVLLNLAISDLLFLITPLWHAHSAANWVFGNAMCKLFTGLYHIGVFGGIFPIILLTID 105
Qy 138 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPIFPRG 197
Db 106 RYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPIFPRG 165
Qy 198 WNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHRVAVRVIPTIMIVYFLFWT 257
Db 166 WNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHRVAVRVIPTIMIVYFLFWT 225
Qy 258 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 317
Db 226 PYNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCNPIIYAFVGEKFRSLFH 285
Qy 318 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 361
Db 286 IALGCRITAPLOKPVCGGPGVRPGKNNKVVTTQGLLDGRGKGSIG 329

RESULT 12
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4
Query Match 83.8%; Score 1651.5; DB 1; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.3e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
Qy 1 MLSTSRIRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSIVFIFGVGN 60
Db 1 MLSTSRIRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSIVFIFGVGN 60
Qy 61 MLVLLINCKLCKLTDIYLLNLAIISDLLFLITPLWHAHSAANWVFGNAMCKLFTGLY 120
Db 61 MLVLLINCKLCKLTDIYLLNLAIISDLLFLITPLWHAHSAANWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
Qy 181 CQKEDSVYVCGPIFPRGNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHR 240
Db 181 CQKEDSVYVCGPIFPRGNNFHTIMRNILGLVLPVLLIMVTCYSGILKTLRCNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLFWTTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCC 300
Db 241 AVRVIPTIMIVYFLFWTTPYNIIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCC 300
Qy 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
Db 301 NPIIYAFVGEKFRRLSVFRKHITKRFCQKCPV 334
RESULT 13
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; APPLICANT: PROTEIN RECEPTORS

; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,669
 ; FILING DATE: May 25, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Neeley, Richard
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: UCAL-237/01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5000
 ; TELEFAX: 415-857-0663
 ; TELEX: 380816COOLEYPA
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-669-4

Query Match 83.8%; Score 1651.5; DB 3; Length 360;
 Best Local Similarity 95.5%; Pred. No. 1.3e-124;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

| | | | |
|----|-----|---|-----|
| QY | 1 | MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVFIIFGVGN | 60 |
| Db | 1 | MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVFIIFGVGN | 60 |
| QY | 61 | MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| Db | 61 | MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| QY | 121 | HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTGVTTSVITLWVAFASVPGIIFTK | 180 |
| Db | 121 | HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTGVTTSVITLWVAFASVPGIIFTK | 180 |
| QY | 181 | CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKRHR | 240 |
| Db | 181 | CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKRHR | 240 |
| QY | 241 | AVRVIPTIMIVYFLWTPYNYIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI | 300 |
| Db | 241 | AVRVIPTIMIVYFLWTPYNYIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI | 300 |
| QY | 301 | NPITIAVFGKEFR---SLF---HIALG-CRIAPL 327 | |
| Db | 301 | NPITIAVFGKEFR---SLF---HIALG-CRIAPL 327 | |

RESULT 14
 US-09-045-583-50
 ; Sequence 50, Application US/09045583
 ; Patent No. 6287805
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street

; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNI-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 360 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-09-045-583-50

Query Match 83.8%; Score 1651.5; DB 3; Length 360;
 Best Local Similarity 95.5%; Pred. No. 1.3e-124;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

| | | | |
|----|-----|---|-----|
| QY | 1 | MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVFIIFGVGN | 60 |
| Db | 1 | MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSILVFIIFGVGN | 60 |
| QY | 61 | MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| Db | 61 | MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| QY | 121 | HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTGVTTSVITLWVAFASVPGIIFTK | 180 |
| Db | 121 | HIGYFGGIFILLITIDRYLAIVHAVFALKARTVTGVTTSVITLWVAFASVPGIIFTK | 180 |
| QY | 181 | CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKRHR | 240 |
| Db | 181 | CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKRHR | 240 |
| QY | 241 | AVRVIPTIMIVYFLWTPYNYIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI | 300 |
| Db | 241 | AVRVIPTIMIVYFLWTPYNYIVILLNTFQEFFGLSNCESTSQLDOATQVTTGLMTHCCI | 300 |
| QY | 301 | NPITIAVFGKEFR---SLF---HIALG-CRIAPL 327 | |
| Db | 301 | NPITIAVFGKEFR---SLF---HIALG-CRIAPL 327 | |

RESULT 15
 US-09-534-185-50
 ; Sequence 50, Application US/09534185
 ; Patent No. 6403767
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
 ; Heptahelical Receptor Superfamily and Uses
 ; Therefor
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 83.8%; Score 1651.5; DB 4; Length 360;
Best Local Similarity 95.5%; Pred. No. 1.3e-124;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
QY 1 MLSTSRSRFRNTNSESSEVTFDDYDYGAPCHKFDVKQIGAOQLLPPLXSLVIFGFGVGN 60
DB 1 MLSTSRSRFRNTNSESSEVTFDDYDYGAPCHKFDVKQIGAOQLLPPLXSLVIFGFGVGN 60
QY 61 MLVVLILINCKLKLCTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKLCTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIVHAVPALKARTVFGVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIVHAVPALKARTVFGVTSVITLWVAFASVPGIIFTK 180
QY 181 COKEDSVYVCGPYPPRCMNNFHTMRNIGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 COKEDSVYVCGPYPPRCMNNFHTMRNIGLVLPLLIMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSOLDQATQVTTILGTHCCI 300
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQFFGLSNCESTSOLDQATQVTTILGTHCCI 300
QY 301 NPITYAFVGEKFR---SLF---HIALG-CRIAPL 327
DB 301 NPITYAFVGEKFRYLSVFFRKHKITKRFCKQCPV 334

Search completed: June 9, 2005, 16:50:10
Job time : 32.0817 secs

| | | | | | | |
|----|------|-------|-----|----|-------------------|--------------------|
| 1 | 1970 | 100.0 | 374 | 10 | US-09-893-512-13 | Sequence 13, Appl |
| 2 | 1970 | 100.0 | 374 | 14 | US-10-039-659-14 | Sequence 14, Appl |
| 3 | 1970 | 100.0 | 374 | 14 | US-10-239-423-63 | Sequence 63, Appl |
| 4 | 1970 | 100.0 | 374 | 16 | US-10-754-071-14 | Sequence 14, Appl |
| 5 | 1970 | 100.0 | 374 | 16 | US-10-741-601-287 | Sequence 287, Appl |
| 6 | 1970 | 100.0 | 374 | 16 | US-10-791-592-2 | Sequence 2, Appl |
| 7 | 1970 | 100.0 | 374 | 16 | US-10-791-166-2 | Sequence 2, Appl |
| 8 | 1970 | 100.0 | 374 | 17 | US-10-759-860-14 | Sequence 14, Appl |
| 9 | 1970 | 100.0 | 374 | 17 | US-10-799-736-13 | Sequence 13, Appl |
| 10 | 1823 | 92.5 | 344 | 9 | US-09-779-879A-9 | Sequence 9, Appl |
| 11 | 1823 | 92.5 | 344 | 9 | US-09-779-880A-9 | Sequence 9, Appl |

| | | | | | | |
|----|------|-------|-----|----|-------------------|--------------------|
| 1 | 1970 | 100.0 | 374 | 10 | US-09-893-512-13 | Sequence 13, Appl |
| 2 | 1970 | 100.0 | 374 | 14 | US-10-039-659-14 | Sequence 14, Appl |
| 3 | 1970 | 100.0 | 374 | 14 | US-10-239-423-63 | Sequence 63, Appl |
| 4 | 1970 | 100.0 | 374 | 16 | US-10-754-071-14 | Sequence 14, Appl |
| 5 | 1970 | 100.0 | 374 | 16 | US-10-741-601-287 | Sequence 287, Appl |
| 6 | 1970 | 100.0 | 374 | 16 | US-10-791-592-2 | Sequence 2, Appl |
| 7 | 1970 | 100.0 | 374 | 16 | US-10-791-166-2 | Sequence 2, Appl |
| 8 | 1970 | 100.0 | 374 | 17 | US-10-759-860-14 | Sequence 14, Appl |
| 9 | 1970 | 100.0 | 374 | 17 | US-10-799-736-13 | Sequence 13, Appl |
| 10 | 1823 | 92.5 | 344 | 9 | US-09-779-879A-9 | Sequence 9, Appl |
| 11 | 1823 | 92.5 | 344 | 9 | US-09-779-880A-9 | Sequence 9, Appl |

Db 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVPASVPGIIFTK 180
Qy 181 CQKEDSVVYCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240
Db 181 CQKEDSVVYCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240
Qy 241 AVRVIETIMIVYFLEWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Db 241 AVRVIETIMIVYFLEWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Qy 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360
Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374

RESULT 2

US-10-039-659-14
; Sequence 14, Application US/10039659
; Publication No. US20030018167A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; Gish, Kurt C.
; Schall, Thomas J.
; Vicari, Alain P.
; Zlotnick, Albert
; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/039,659
; FILING DATE: 03-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/887,977
; FILING DATE: 03-JUL-1997
; APPLICATION NUMBER: US 60/021,644
; FILING DATE: 05-JUL-1996
; APPLICATION NUMBER: US 60/028,329
; FILING DATE: 11-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0589K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9192
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14
Query Match 100.0%; Score 1970; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60
Db 1 MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVPASVPGIIFTK 180
Db 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTGVTSTVITLWVAVPASVPGIIFTK 180
Qy 181 CQKEDSVVYCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240
Db 181 CQKEDSVVYCGPYFPRGWNFNHIMRNILGLVPLLIWVICYSGILKTLRLCRNEKKRHR 240
Qy 241 AVRVIETIMIVYFLEWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Db 241 AVRVIETIMIVYFLEWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
Qy 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360
Db 301 NPIIYAFVGEKFRSLFHIALGCRIPLOKPVCGGPGVRPGKNVKTQTQGLLDGRGKSKI 360
Qy 361 GRAPEASLQDKEGA 374
Db 361 GRAPEASLQDKEGA 374
RESULT 3
US-10-239-423-63
; Sequence 63, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
; APPLICANT: HEITLAND, Alekandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammatory Diseases,
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-63
Query Match 100.0%; Score 1970; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60
Db 1 MLSTSRSRFRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFFGVGN 60
Qy 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120

```

Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Db      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Qy      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Db      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 4

US-10-754-071-14

; Sequence 14, Application US/10754071

; Publication No. US20040137578A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Wei

; APPLICANT: Gish, Kurt C.

; APPLICANT: Schall, Thomas J.

; APPLICANT: Vicari, Alain P.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Chemokine TECK Polypeptides

; FILE REFERENCE: DK0589KIC US

; CURRENT APPLICATION NUMBER: US/10754,071

; CURRENT FILING DATE: 2004-01-07

; PRIOR APPLICATION NUMBER: US 10/039,659

; PRIOR FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: US 08/887,977

; PRIOR FILING DATE: 1997-07-03

; PRIOR APPLICATION NUMBER: US 60/021,664

; PRIOR FILING DATE: 1996-07-05

; PRIOR APPLICATION NUMBER: US 60/028,329

; PRIOR FILING DATE: 1996-10-11

; PRIOR APPLICATION NUMBER: US 60/048,593

; PRIOR FILING DATE: 1997-06-04

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-754-071-14

```

Query Match      100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Db      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Qy      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240

```

```

Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Db      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Qy      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Db      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 5

US-10-741-601-287

; Sequence 287, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 287

; LENGTH: 374

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-601-287

```

Query Match      100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Db      1  MLSTSRSRFRINTNESGEEVTFDFDYDGAPCHKFDVKQIGAQLLPPLYSILVFIFFGVGN 60
Qy      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVLLILNCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGYFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Db      181  COKEDSVVCGPYPPRGWNNFHTIMRNILGLVLPDLLIMVICYSGILKTLRCRNEKKRHR 240
Qy      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Db      241  AVRVIPTIMIVYFLFWTPYNIIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLDGRGKSI 300
Qy      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Db      301  NPITIAVFGKFRSLFHIALGCRIPALQKPVCGGPGVRPGKNVKTQGLDGRGKSI 360
Qy      361  GRAPEASLQDKEGA 374
Db      361  GRAPEASLQDKEGA 374

```

RESULT 6

US-10-791-592-2

; Sequence 2, Application US/10791592

; Publication No. US20040219644A1

; GENERAL INFORMATION:

APPLICANT: Charo, Israel
Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/791,592
FILING DATE: 01-Mar-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-592-2

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQFVGN 60
QY 61 MLVVILINCKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVILINCKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICSGLIKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICSGLIKTLRCNEKKRHR 240
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAVGKFSLFHIALGCRITAPLQKPCGPGVPRGNKVVTQGLLDGRGKSI 360
DB 301 NPIIYAVGKFSLFHIALGCRITAPLQKPCGPGVPRGNKVVTQGLLDGRGKSI 360
QY 361 GRAPEASLODKEGA 374
|||||

Db 361 GRAPEASLODKEGA 374
RESULT 7
US-10-791-166-2
; Sequence 2, Application US/10791166
; Publication No. US20040223968A1
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/791,166
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-791-166-2

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.4e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPPLYSLVFIQFVGN 60
QY 61 MLVVILINCKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVILINCKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICSGLIKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYPPRGNNFHTIMRNILGLVPLLIWVICSGLIKTLRCNEKKRHR 240
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
|||||

Db 241 AVRVTIMIVYFLFTWTPYNIIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374
 RESULT 8
 US-10-759-860-14
 ; Sequence 14, Application US/10759860
 ; Publication No. US2005007490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Wei
 ; APPLICANT: Gish, Kurt C.
 ; APPLICANT: Schall, Thomas J.
 ; APPLICANT: Vicari, Alain P.
 ; TITLE OF INVENTION: Methods for using chemokine TECK
 ; FILE REFERENCE: DX0589K1D US
 ; CURRENT APPLICATION NUMBER: US/10759,860
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: US 10/039,659
 ; PRIOR FILING DATE: 2002-01-03
 ; PRIOR APPLICATION NUMBER: US 08/887,977
 ; PRIOR FILING DATE: 1997-07-03
 ; PRIOR APPLICATION NUMBER: US 60/021,664
 ; PRIOR FILING DATE: 1996-07-05
 ; PRIOR APPLICATION NUMBER: US 60/028,329
 ; PRIOR FILING DATE: 1996-10-11
 ; PRIOR APPLICATION NUMBER: US 60/048,593
 ; PRIOR FILING DATE: 1997-06-04
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-759-860-14
 Query Match 100.0%; Score 1970; DB 17; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLSTSRSRFRINTNESGEVTTFFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFTFGFVGN 60
 Db 1 MLSTSRSRFRINTNESGEVTTFFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFTFGFVGN 60
 Qy 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYPRGWNFNHTMRNIGLVPLLIWVCYSGILKTLRCRNEKGRHR 240
 Db 181 CQKEDSVYVCGPYPRGWNFNHTMRNIGLVPLLIWVCYSGILKTLRCRNEKGRHR 240
 Qy 241 AVRVTIMIVYFLFTWTPYNIIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 Db 241 AVRVTIMIVYFLFTWTPYNIIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374
 RESULT 10
 US-09-779-879A-9
 ; Sequence 9, Application US/09779879A
 ; Patent No. US20020048786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Roschke, Viktor
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

Db 361 GRAPEASLQDKEGA 374
 RESULT 9
 US-10-799-736-13
 ; Sequence 13, Application US/10799736
 ; Publication No. US20050118675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OWMAN, CHRISTER
 ; TITLE OF INVENTION: HEPTAHMELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
 ; TITLE OF INVENTION: RECEPTOR
 ; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/10799,736
 ; CURRENT FILING DATE: 2004-03-15
 ; PRIOR APPLICATION NUMBER: US/09/893,512
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 60/061,789
 ; PRIOR FILING DATE: 1997-10-14
 ; PRIOR APPLICATION NUMBER: 60/081,958
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 09/170,069
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-799-736-13
 Query Match 100.0%; Score 1970; DB 17; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.4e-163;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLSTSRSRFRINTNESGEVTTFFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFTFGFVGN 60
 Db 1 MLSTSRSRFRINTNESGEVTTFFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFTFGFVGN 60
 Qy 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKKCLTDIYLLNLAISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYPRGWNFNHTMRNIGLVPLLIWVCYSGILKTLRCRNEKGRHR 240
 Db 181 CQKEDSVYVCGPYPRGWNFNHTMRNIGLVPLLIWVCYSGILKTLRCRNEKGRHR 240
 Qy 241 AVRVTIMIVYFLFTWTPYNIIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 Db 241 AVRVTIMIVYFLFTWTPYNIIVLLNTFQBFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 Qy 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGPGVPRGNVKTQGLDGRGKSKI 360
 Qy 361 GRAPEASLQDKEGA 374
 Db 361 GRAPEASLQDKEGA 374
 RESULT 10
 US-09-779-879A-9
 ; Sequence 9, Application US/09779879A
 ; Patent No. US20020048786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, Craig A.
 ; APPLICANT: Roschke, Viktor
 ; APPLICANT: Li, Yi
 ; APPLICANT: Ruben, Steven, M.
 ; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10

FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 77
DB 1 EEVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 60
QY 78 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137
DB 61 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120
QY 138 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 197
DB 121 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 180
QY 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 257
DB 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 240
QY 258 PYNIVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 317
DB 241 PYNIVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 300
QY 318 IALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKKSIG 361
DB 301 IALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKKSIG 344

RESULT 11
US-09-779-880A-9
; Sequence 9, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-9

Query Match 92.5%; Score 1823; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 77
DB 1 EEVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 60
QY 78 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137
DB 61 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120
QY 138 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 197
DB 121 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 180
QY 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 257
DB 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 240
QY 258 PYNIVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 317
DB 241 PYNIVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLPH 300
QY 318 IALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKKSIG 361
DB 301 IALGCRIPALQKPVCGPGVRPGKNVKVTTQGLLDGRGKKSIG 344

RESULT 12
US-10-232-686-9
; Sequence 9, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-232-686-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EVVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 77
DB 1 EEVTFDDYDYGAPCHKFDVKQIGAQLLPPLYSLVFI FGVGNMVLVLLINCKKLCLT 60
QY 78 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 137
DB 61 DIYLLNLAI SDDLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGIFFIILLTID 120
QY 138 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 197
DB 121 RYLAIHVAHFALKARTVTFTGVVTSVITLWVAVFASVPGIIFTKCKEDSVVYCGPYFPRG 180
QY 198 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 257
DB 181 WNNFHTIMRNILGLVLP LLIMVICYSGILKTLRLCRNEKRRHRAVRVIFTIMIVYFLFWT 240

Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300
Qy 318 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 361
Db 301 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 344

RESULT 13

US-10-067-800-9
; Sequence 9, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.1150001
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTTFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGNMVLVILINCKKLKLT 77
Db 1 BEVTTTFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGNMVLVILINCKKLKLT 60
Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
Qy 138 RYLAIVHAVFALKARTVTGVTTSVITWLVAVFASVPGIIFTKCKEDSVVVCPPYPRG 197
Db 121 RYLAIVHAVFALKARTVTGVTTSVITWLVAVFASVPGIIFTKCKEDSVVVCPPYPRG 180
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 257
Db 181 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 240
Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300
Qy 318 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 361
Db 301 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 344

RESULT 14

US-10-135-839-9

; Sequence 9, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-9

Query Match 92.5%; Score 1823; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 2e-150;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 BEVTTTFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGNMVLVILINCKKLKLT 77
Db 1 BEVTTTFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVGNMVLVILINCKKLKLT 60
Qy 78 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db 61 DIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120
Qy 138 RYLAIVHAVFALKARTVTGVTTSVITWLVAVFASVPGIIFTKCKEDSVVVCPPYPRG 197
Db 121 RYLAIVHAVFALKARTVTGVTTSVITWLVAVFASVPGIIFTKCKEDSVVVCPPYPRG 180
Qy 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 257
Db 181 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRVIPTIMIYVFLFWT 240
Qy 258 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 317
Db 241 PYNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFRSLFH 300
Qy 318 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 361
Db 301 IALGCRITAPLQKPVCGGPGVRPGKRVKVTQTGLDGRGKGSIG 344

RESULT 15

US-09-725-285-9
; Sequence 9, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-725-285-9

Query Match      87.7%; Score 1727.5; DB 9; Length 329;
Best Local Similarity 95.6%; Pred. No. 4e-142;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 18 EEVTFEDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMLVVLIIINCKKXCLT 77
Db 1 EEVTFEDYDYGAPCHKFDVKQIGAQLLPPLYSLSVFIFFGVGNMLVVLIIINCKKXCLT 60

QY 78 DIYLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
Db 61 DIYLLNLAIISDLLFLITPLWAHSAANEWVFGNAMCKLFTGLYHI----- 105

QY 138 RYLAIYHVAEPALKARTVTFGVTSVITLWAVFASVPGIIFTCKOKEDSVVCGPYPPRG 197
Db 106 RYLAIYHVAEPALKARTVTFGVTSVITLWAVFASVPGIIFTCKOKEDSVVCGPYPPRG 165

QY 198 WNNFHTIMRNILGIVLPLLIIVICYSGLIKTLRCRNEKKRHRVRIFTIMIVYFLFWT 257
Db 166 WNNFHTIMRNILGIVLPLLIIVICYSGLIKTLRCRNEKKRHRVRIFTIMIVYFLFWT 225

QY 258 PYNIVILLNTFQBFPGLSNCESTSOLDQATQVTETLGWTHCCINPIIYAFVGEKFRSLFH 317
Db 226 PYNIVILLNTFQBFPGLSNCESTSOLDQATQVTETLGWTHCCINPIIYAFVGEKFRSLFH 285

QY 318 IALGCRITAPLQKPVCGGPGVPRGKNVKTQTQGLDGRGKKSIG 361
Db 286 IALGCRITAPLQKPVCGGPGVPRGKNVKTQTQGLDGRGKKSIG 329
```

Search completed: June 9, 2005, 17:06:37
Job time : 106.455 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:27:48 ; Search time 111.826 Seconds
(without alignments)
1245.097 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900
Sequence: 1 MLSTSRFRIRNTNBSGEV.....DGVSTNTPSTGRQSVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 1900 | 100.0 | 360 | 2 AAR79166 | Aar79166 Human mon |
| 2 | 1900 | 100.0 | 360 | 2 AAW35833 | Aaw35833 Human mon |
| 3 | 1900 | 100.0 | 360 | 4 AAG80108 | Aag80108 Human CCR |
| 4 | 1900 | 100.0 | 360 | 4 AAU07614 | Aau07614 Human wil |
| 5 | 1900 | 100.0 | 360 | 6 ABP97725 | Abp97725 Amino aci |
| 6 | 1900 | 100.0 | 360 | 6 ABP81987 | Abp81987 Human C-C |
| 7 | 1900 | 100.0 | 360 | 8 ADM67225 | Adm67225 Human aci |
| 8 | 1900 | 100.0 | 360 | 8 ADL82831 | Adl82831 Human PRO |
| 9 | 1899 | 99.9 | 360 | 4 AAU07613 | Aau07613 Human CCR |
| 10 | 1894 | 99.7 | 360 | 4 ABB56340 | Abb56340 Non-endog |
| 11 | 1838 | 96.7 | 347 | 7 ADF56627 | Adf56627 Partial h |
| 12 | 1651.5 | 86.9 | 374 | 2 AAR79165 | Aar79165 Human mon |
| 13 | 1651.5 | 86.9 | 374 | 4 AAG80107 | Aag80107 Human CCR |
| 14 | 1651.5 | 86.9 | 374 | 6 ABU09083 | Abu09083 Human che |
| 15 | 1651.5 | 86.9 | 374 | 7 ADD44861 | Add44861 Human pro |
| 16 | 1651.5 | 86.9 | 374 | 7 ADD44865 | Add44865 Human pro |
| 17 | 1651.5 | 86.9 | 374 | 7 ADP65146 | Adp65146 Human che |
| 18 | 1651.5 | 86.9 | 374 | 8 ADO29221 | Ado29221 Human GPC |
| 19 | 1651.5 | 86.9 | 374 | 8 ADQ67847 | Adq67847 Human che |
| 20 | 1568.5 | 82.6 | 344 | 5 ABG92881 | Abg92881 Class I r |
| 21 | 1568.5 | 82.6 | 344 | 6 ABU61655 | Abu61655 Human mon |
| 22 | 1568.5 | 82.6 | 344 | 7 ADP72129 | Adp72129 Human G-p |
| 23 | 1568.5 | 82.6 | 344 | 8 ADP86217 | Adp86217 Human MCP |
| 24 | 1535 | 80.8 | 373 | 8 ADM67224 | Adm67224 Murine ad |
| 25 | 1535 | 80.8 | 373 | 8 ADO29222 | Ado29222 Mouse GPC |

| | | | | | |
|----|------|------|-----|------------|--------------------|
| 26 | 1535 | 80.8 | 373 | 8 ADP74040 | Adp74040 Murine CC |
| 27 | 1473 | 77.5 | 329 | 4 AAB46859 | Aab46859 Human MCP |
| 28 | 1473 | 77.5 | 329 | 5 ABB81055 | Abb81055 Human MCP |
| 29 | 1473 | 77.5 | 329 | 8 ADR16266 | Adr16266 Human MCP |
| 30 | 1396 | 73.5 | 354 | 8 ADO29228 | Ado29228 Mouse GPC |
| 31 | 1386 | 72.9 | 354 | 2 AAW54037 | Aaw54037 Mouse CC- |
| 32 | 1386 | 72.9 | 354 | 7 ADD44859 | Add44859 Rat Prote |
| 33 | 1386 | 72.9 | 354 | 7 ADD44863 | Add44863 Rat Prote |
| 34 | 1371 | 72.2 | 352 | 4 AAG79089 | Aag79089 Amino aci |
| 35 | 1364 | 71.8 | 352 | 2 AAW27407 | Aaw27407 Human CCR |
| 36 | 1364 | 71.8 | 352 | 2 AAW27123 | Aaw27123 Human che |
| 37 | 1364 | 71.8 | 352 | 2 AAW27125 | Aaw27125 Macaque c |
| 38 | 1364 | 71.8 | 352 | 2 AAW23835 | Aaw23835 Human CC |
| 39 | 1364 | 71.8 | 352 | 2 AAW88232 | Aaw88232 HIV-1 co- |
| 40 | 1364 | 71.8 | 352 | 4 AAG80111 | Aag80111 Human CCR |
| 41 | 1364 | 71.8 | 352 | 4 AAE04321 | Aae04321 Human che |
| 42 | 1364 | 71.8 | 352 | 4 AAB83354 | Aab83354 Human CCR |
| 43 | 1364 | 71.8 | 352 | 4 AAB82948 | Aab82948 Human HIV |
| 44 | 1364 | 71.8 | 352 | 5 AAM52828 | Aam52828 Human CC |
| 45 | 1364 | 71.8 | 352 | 5 ABB08343 | Abb08343 Human che |

ALIGNMENTS

RESULT 1
AAR79166
ID AAR79166 standard; protein; 360 AA.
XX
AC AAR79166;
XX
DT 25-MAR-2003 (revised)
DT 29-DEC-1995 (first entry)
XX
DE Human monocyte chemoattractant protein-1 receptor MCP-1RB.
XX
KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..48 /label= extracellular
FT Domain 49..70 /label= transmembrane
FT Domain 80..700 /label= transmembrane
FT Domain 115..136 /label= transmembrane
FT Domain 154..178 /label= transmembrane
FT Domain 204..231 /label= transmembrane
FT Domain 244..268 /label= transmembrane
FT Domain 295..313 /label= transmembrane
FT Domain 314..360 /label= transmembrane
FT Region /label= carboxyl tail
XX
WO9519436-A1.
XX
PD 20-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US0000476.
XX
PR 13-JAN-1994; 94US-00182962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Charo I, Coughlin S;
XX
DR WPI; 1995-263866/34.

DR N-PSDB; AAQ96298.
 XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocyte infiltrates.
 XX
 PS Claim 2; Fig 2; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obtd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct FN
 CC field.)
 XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
 QY 121 HIGYFGIGFIIILLTIDRYLAIHVAVFALKARTVTFGVTSVITWLVAVPASVPGIIFTK 180
 DB 121 HIGYFGIGFIIILLTIDRYLAIHVAVFALKARTVTFGVTSVITWLVAVPASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
 DB 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 2
 AAW35833
 ID AAW35833 standard; protein; 360 AA.
 AC AAW35833;
 XX
 XX 27-FEB-1998 (first entry)
 DT Human monocyte chemoattractant protein 1 receptor.
 DE
 XX Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;
 XX inflammatory disease; viral; allergy; diabetes.
 XX

OS Homo sapiens.
 XX JF09238688-A.
 PN 16-SEP-1997.
 PD 11-MAR-1996; 96JP-00053574.
 XX 11-MAR-1996; 96JP-00053574.
 PR (TAKE) TAKEDA CHEM IND LTD.
 PA WPI; 1997-506557/47.
 XX N-PSDB; AAT96976.
 DR DNA encoding human monocyte chemoattractant protein 1 receptor - used to
 PT treat tumours and inflammatory, viral, infectious, allergic, diabetic and
 PT central nervous system diseases.
 PS Disclosure; Page 12-14; 15pp; Japanese.
 XX

CC The present sequence represents human monocyte chemoattractant protein 1
 CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA are
 CC used for the prevention and treatment of tumours and inflammatory, viral,
 CC infectious, allergic, diabetic and central nervous system diseases
 CC
 XX Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGVGN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITPLWAHSAANEVWFGNAMCKLFTGLY 120
 QY 121 HIGYFGIGFIIILLTIDRYLAIHVAVFALKARTVTFGVTSVITWLVAVPASVPGIIFTK 180
 DB 121 HIGYFGIGFIIILLTIDRYLAIHVAVFALKARTVTFGVTSVITWLVAVPASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
 DB 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 3
 AAG80108
 ID AAG80108 standard; protein; 360 AA.
 AC AAG80108;
 XX
 XX 17-JAN-2002 (first entry)
 DT Human CCR2b protein.
 DE
 XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 XX chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 XX anti-inflammatory; antiasthmatic; immunosuppressive; dermatological;
 XX antirheumatic; antiarthritic.
 XX

| | |
|---------------------------|--|
| OS | Homo sapiens. |
| XX | |
| PN | WO200172830-A2. |
| XX | |
| PD | 04-OCT-2001. |
| XX | |
| PF | 02-APR-2001; 2001WO-EP003708. |
| XX | |
| PR | 31-MAR-2000; 2000DE-01016013. |
| XX | (IPFP-) IPF PHARM GMBH. |
| PA | (FORS/) FORSSWANN U. |
| XX | |
| PI | Forsmann W, Adermann K, Heitland A, Spodsberg N; |
| XX | |
| DR | WPI; 2001-626256/72. |
| XX | |
| PT | Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors. |
| PT | |
| XX | |
| PS | Disclosure; Page 9; 26pp; German. |
| XX | |
| CC | This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AAG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention |
| XX | |
| SQ | Sequence 360 AA; |
| | |
| Query Match | 100.0%; Score 1900; DB 4; Length 360; |
| Best Local Similarity | 100.0%; Pred. No. 1.9e-206; |
| Matches 360; Conservative | 0; Mismatches 0; Indels 0; Gaps 0 |
| | |
| Qy | 1 MLSTSRGRFRINTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLLPPLYSLVTFPGFVGN 60 |
| Db | 1 MLSTSRGRFRINTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLLPPLYSLVTFPGFVGN 60 |
| | |
| Qy | 61 MLVVLLINCKKACLTDIYLLNLAIISDLLFLITLPLWAHSAAENEWFGNAWKLFCTGLY 120 |
| Db | 61 MLVVLLINCKKACLTDIYLLNLAIISDLLFLITLPLWAHSAAENEWFGNAWKLFCTGLY 120 |
| | |
| Qy | 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVTVTSITWLVAVFASVPGIIFTK 180 |
| Db | 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVTVTSITWLVAVFASVPGIIFTK 180 |
| | |
| Qy | 181 CQKEDSVVCGPYPPRGNNPHFTIMRNLTGLVLPLLIMVICYSGILKTLLCRNEKKRRH 240 |
| Db | 181 CQKEDSVVCGPYPPRGNNPHFTIMRNLTGLVLPLLIMVICYSGILKTLLCRNEKKRRH 240 |
| | |
| Qy | 241 AVRVIPTMIVYFLFWTPYNYVILLNTFOBPPGISNCBSTSOLDOATQVTTGLGTHCCI 300 |
| Db | 241 AVRVIPTMIVYFLFWTPYNYVILLNTFOBPPGISNCBSTSOLDOATQVTTGLGTHCCI 300 |
| | |
| Qy | 301 NPITIYAVGEKFRRYLSVFFRKHIITKRCPCQCPFYRETVDGVTSINTPSTGEOEVSAGL 360 |
| Db | 301 NPITIYAVGEKFRRYLSVFFRKHIITKRCPCQCPFYRETVDGVTSINTPSTGEOEVSAGL 360 |
| | |
| RESULT 4 | |
| AU07614 | |

Db 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSA 360
 Db 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSA 360
 RESULT 5
 ABP97725
 ID ABP97725 standard; protein; 360 AA.
 XX
 AC ABP97725;
 XX
 DT 28-MAY-2003 (first entry)
 DE Amino acid sequence of human chemokine receptor CCR2.
 XX
 KW Human; chemokine receptor; CCR2; viral infection; surface protein;
 KW respiratory virus infection; respiratory syncytial virus infection;
 KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.
 XX
 OS Homo sapiens.
 XX
 PN WO2003014153-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 12-AUG-2002; 2002WO-CA001248.
 XX
 PR 10-AUG-2001; 2001US-0311088P.
 XX
 PA (TOPI-) TOPIGEN PHARM INC.
 XX
 PI Renzi P, Zemzoui K;
 DR WPI; 2003-256541/25.
 DR N-PSDB; ABZ68878.
 XX
 PT Modulating viral infection of a cell, for treating or preventing
 PT respiratory virus infections, bronchitis, pneumonia or asthma, by
 PT modulating a binding interaction between a cell chemokine-receptor and a
 PT surface protein of the virus.
 XX
 PS Disclosure; Page 82-84; 120pp; English.
 XX
 CC The present sequence represents human chemokine receptor CCR2. The
 CC specification describes a method for modulating viral infection of a
 CC cell. The method comprises modulating a binding interaction between a
 CC cell chemokine-receptor and a surface protein of the virus. The proviso
 CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
 CC not HIV. The method is useful for treating or preventing respiratory
 CC virus infection in vertebrates, more particularly respiratory syncytial
 CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
 CC bronchitis, pneumonia or asthma
 XX
 SQ Sequence 360 AA;
 Query Match 100.0%; Score 1900; DB 6; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLSTSRSRFRNTNNEGSEVTFPDYDGAPCHKFDVKQIGALLPPLYSLVIFFGVGN 60
 Db 1 MLSTSRSRFRNTNNEGSEVTFPDYDGAPCHKFDVKQIGALLPPLYSLVIFFGVGN 60
 QY 61 MLVVLLINCKKGLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 Db 61 MLVVLLINCKKGLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
 QY 121 HGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVWTSVITLWVAVFASVPGIIFTK 180
 Db 121 HGVFGGIFPIILLTIDRYLAIVHAVFALKARTVTFGVWTSVITLWVAVFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVPLLIWVICYSGLKTLRCRNEKKRHR 240
 Db 181 CQKEDSVYVCGPYFPRGWNHFTIMRNILGLVPLLIWVICYSGLKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300
 Db 241 AVRVIPTIMIVYFLWTPYNNIVILLNTFQBFGLSNCESTSLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSA 360
 Db 301 NPIIYAVGKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPTSGQEVSA 360
 RESULT 6
 ABP81987
 ID ABP81987 standard; protein; 360 AA.
 XX
 AC ABP81987;
 XX
 DT 04-MAR-2003 (first entry)
 DE Human C-C chemokine receptor 2 protein SEQ ID NO:460.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burmer GC, Roush CL, Brown JP;
 DR WPI; 2003-046718/04.
 DR N-PSDB; ABZ42835.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Disclosure; Fig 1; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 6; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGFGVN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGFGVN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIPFIILLTIDRYLAIVHAFVFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 DB 121 HIGYFGGIPFIILLTIDRYLAIVHAFVFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVTCYSGILKTLRCNEKKRHR 240
 DB 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVTCYSGILKTLRCNEKKRHR 240
 QY 241 AVRVIPTIMLVYFLFWTPYNNIVLLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMLVYFLFWTPYNNIVLLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360
 DB 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 7
 ADM67225
 ID ADM67225 standard; protein; 360 AA.
 XX
 AC ADM67225;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human adipocyte specific chemokine (C-C) receptor 2 protein SeqID 579.

DE human; adipocyte specific; adipose tissue; anti-obesity;
 KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
 KW adipogenesis; hypertension; cardiovascular disease; anorectic;
 KW antidiabetic; hypotensive; chemokine (C-C) receptor 2.
 XX
 OS Homo sapiens.
 XX
 PN W02004011618-A2.
 XX
 PD 05-FEB-2004.
 XX
 XX 29-JUL-2003; 2003WO-US023684.
 XX
 PR 29-JUL-2003; 2002US-0398785P.
 PR 12-JUN-2003; 2003US-0478206P.
 XX
 XX (HMGE-) HMGNE INC.
 PA
 XX Chada K, Chouinard R, Ashar H, Sayed AMD;
 PI
 XX

DR WPI; 2004-143846/14.
 DR N-PSDB; ADM66946.
 XX
 PT Identifying adipocyte specific genes, useful for treating obesity or
 PT diabetes, and for identifying drug targets, by differential gene
 PT expression analysis between adipose tissue or stromal vascular tissue of
 PT mice of different genotypes.
 XX
 XX Disclosure; SEQ ID NO 579; 91pp; English.

XX This invention relates to a novel method for identifying genes that are
 CC over-expressed in adipose tissue and as such it provides targets for anti
 CC -obesity pharmaceutical compositions. Specifically, it refers to a high
 CC mobility group I-C protein (HMGI-C) that is associated with obesity and
 CC is epistatic to leptin, furthermore, it refers to the ob gene where an
 CC autosomal recessive trait is linked to obesity and diabetes. The present
 CC invention describes performing differential gene expression analysis
 CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
 CC of any two different mice selected from a group consisting of wild-type,
 CC HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using
 CC this method novel nucleotides and the encoded proteins thereof were
 CC identified that are adipocyte specific, and as such can be used for
 CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
 CC hypertension and cardiovascular disease, as well as screening for
 CC compounds that can modulate or prevent adipogenesis and treat diabetes or
 CC obesity. These compositions exhibit anorectic, antidiabetic and
 CC hypotensive activities. This polypeptide sequence is a human homologue of
 CC a murine adipocyte specific protein sequence of the invention.

XX Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.9e-206;
 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGFGVN 60
 DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDGAPCHKFDVKQIGALLPPLYSILVIFGFGVN 60
 QY 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLCITDIYLLNLAI SDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIPFIILLTIDRYLAIVHAFVFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 DB 121 HIGYFGGIPFIILLTIDRYLAIVHAFVFAKARTVTFGVTSVITLWVAFASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVTCYSGILKTLRCNEKKRHR 240
 DB 181 CQKEDSVYVCGPYPPRGWNNFHTIMRNILGLVPLLIWVTCYSGILKTLRCNEKKRHR 240
 QY 241 AVRVIPTIMLVYFLFWTPYNNIVLLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMLVYFLFWTPYNNIVLLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360
 DB 301 NPIIYAFVGEKFRYLSVFFPRKHITKRCQCPVYRETVDGVTSTNTPSTGQEVSAAGL 360

RESULT 8
 ADL82831
 ID ADL82831 standard; protein; 360 AA.
 XX
 AC ADL82831;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human PRO84690, SEQ ID 33.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; cancer;

KW immune-mediated inflammatory disease; human.

OS Homo sapiens.

XX WO2004024097-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US029097.

XX 16-SEP-2002; 2002US-0411392P.

XX (GETH) GENENTECH INC.

XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI,

PI Wu TD;

XX WPI; 2004-329389/30.

DR N-PSDB; ADL82830.

XX New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.

XX Claim 10; Fig 33; 695pp; English.

XX The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide antigen unresponsiveness, selective IGA deficiency, selective IgM deficiency, selective deficiency of IGA subclasses, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hyperplasia, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.

XX Sequence 360 AA;

Query Match 100.0%; Score 1900; DB 8; Length 360;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFVGN 60

DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFVGN 60

QY 61 MLVVLILINCKLKLCTDIYLLNLAISSLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120

DB 61 MLVVLILINCKLKLCTDIYLLNLAISSLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180

DB 121 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180

QY 181 CQKEDSVYVCGPYFPRGNFNHITMRNLGLVPLIMWICYSGLKTLRLCRNEKKRRH 240

DB 181 CQKEDSVYVCGPYFPRGNFNHITMRNLGLVPLIMWICYSGLKTLRLCRNEKKRRH 240

QY 241 AVRVIPTIMIVFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300

DB 241 AVRVIPTIMIVFLFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAVGKPRYLSVFRKHTKRCQCPVFRVRETVDGVTSTNTPSTGQEVSAGL 360

DB 301 NPIIYAVGKPRYLSVFRKHTKRCQCPVFRVRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 9

ID AAU07613 standard; protein; 360 AA.

XX AAU07613;

XX 04-DEC-2001 (first entry)

XX Human CCR2-64I polymorphic variant polypeptide.

XX Human; CCR2 receptor; CCR2-64I; CCR2-64V; gene therapy; atherosclerosis; single nucleotide polymorphism; hypercholesterolaemia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 64

FT /note= "Wild-type Val is replaced by Ile"

XX WO200162796-A1.

XX 30-AUG-2001.

XX 22-FEB-2001; 2001WO-GB000755.

XX 22-FEB-2000; 2000GB-00004183.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Valdes AM, Groot PHE, Spurr NK;

XX WPI; 2001-550086/61.

XX N-PSDB; AAS12139.

XX Diagnosing atherosclerosis or susceptibility to atherosclerosis in a subject, by determining a single nucleotide polymorphism in specific codon of a polynucleotide encoding human CCR2 receptor in genome of the subject.

XX Claim 1; Page 20; 28pp; English.

XX The invention relates to diagnosing atherosclerosis (or susceptibility to) in a subject by determining expression or activity of the human CCR2-64I polypeptide (a polymorphic variant form of the human CCR2 receptor) or the CCR2-64V polypeptide (human CCR2 receptor), by screening for a single nucleotide polymorphism in codon 64 of the polynucleotide encoding the CCR2 receptor. This results in production of CCR2-64I, whereby polymorphic variants are associated with a lower incidence of atherosclerosis. The presence or amount of CCR2-64I/V in a sample can also be analysed. The sequences of the invention can be used for predicting the response of a patient to drug treatment, for predicting the disease outcome in a patient and also for the production of a treatment for hypercholesterolaemia. The sequence represents the polymorphic variant polypeptide CCR2-64I

XX Sequence 360 AA;

Query Match 99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.9%; Pred. No. 2.4e-206;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFVGN 60

DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGFVGN 60

QY 61 MLVVLILINCKLKLCTDIYLLNLAISSLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120

DB 61 MLVVLILINCKLKLCTDIYLLNLAISSLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180

DB 121 HIGYFGGIFPIILLTIDRYLAIVHAFALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180

QY 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240
 DB 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 10

ABB56340
 ID ABB56340 standard; protein; 360 AA.

XX ABB56340;

DT 18-FEB-2002 (first entry)

DE Non-endogenous human GPCR protein, SEQ ID NO: 473.

KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.

OS Homo sapiens.

XX Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

DR N-PSDB; ABI97976.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.

XX Claim 1; Page 274-275; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR

XX Sequence 360 AA;

XX Query Match

XX Best Local Similarity 99.7%; Score 1894; DB 4; Length 360;

XX Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRGRFIRNTNESGEVTFDFDYDGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60

DB 1 MLSTSRGRFIRNTNESGEVTFDFDYDGAPCHKFDVKQIGQALLPPLYSLVFIQFVGN 60

QY 61 MLVVLILINCKKLCITDIYLLNLAISDLLPLITLPLWAHSAANEWFGNAMCKLFTGLY 120

DB 61 MLVVLILINCKKLCITDIYLLNLAISDLLPLITLPLWAHSAANEWFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFPILLITIDRYLAIVHAVFALFKARTTTFGVVTSVITWLVAVFASVPGIIFTK 180
 DB 121 HIGYFGGIFPILLITIDRYLAIVHAVFALFKARTTTFGVVTSVITWLVAVFASVPGIIFTK 180
 QY 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240
 DB 181 COKEDSVVCGPYPRGWNHFTIMRNILGLVLPILLIMVICYSGILKTLRCRNEKKRHR 240
 QY 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360
 DB 301 NPIIYAFVGEKFRRLYSVFFRKHTKRCCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 11

ADF56627
 ID ADF56627 standard; protein; 347 AA.

XX ADF56627;

DT 12-FEB-2004 (first entry)

DE Partial human monocyte chemoattractant protein 1 receptor.

KW antiasthmatic; cardiac; hypotensive; antiallergic; neuroprotective;
 KW osteopathic; vulnary; gene therapy; asthma; acute heart failure;
 KW hypertension; osteoporosis; allergy; dementia; ulcer; human;
 KW G protein coupled receptor; HGBER32;
 KW monocyte chemoattractant protein 1 receptor.

XX Homo sapiens.

XX US2003165901-A1.

XX 04-SEP-2003.

XX 21-JUN-2002; 2002US-00176078.

XX 05-JUN-1995; 95US-00461244.

XX 25-JUN-1998; 98US-00104792.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Soppet DR, Li Y, Rosen CA, Ruben SM;

XX WPI; 2003-898052/82.

XX New polynucleotide, useful for preparing a composition for diagnosing or
 PT treating e.g. asthma, acute heart failure, hypertension, osteoporosis,
 PT allergies, dementia or ulcers.

XX Disclosure; SEQ ID NO 3; 28pp; English.

XX The invention describes an isolated polynucleotide comprising a sequence
 CC encoding the polypeptide comprising a 355 residue amino acid sequence,
 CC given in the specification, a sequence encoding the polypeptide expressed
 CC by the DNA contained in ATCC Deposit No. 97187, a sequence that
 CC hybridises with, or that is at least 70 % identical to them, or a
 CC sequence fragment of them. The polynucleotide is useful for preparing a
 CC composition for diagnosing or treating asthma, acute heart failure, a
 CC hypertension, osteoporosis, allergies, dementia or ulcers. This is the
 CC amino acid sequence of human monocyte chemoattractant protein 1 receptor
 CC starting at residue 40 and used in a comparison with human G protein
 CC coupled receptor HGBER32.

XX Sequence 347 AA;

XX Query Match

XX Best Local Similarity 96.7%; Score 1838; DB 7; Length 347;

XX Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 NESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLVSLVIFGVGNMVLILINCKKL 73
 DB 1 NESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLVSLVIFGVGNMVLILINCKKL 60
 QY 74 KCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHICYGFGIPIIL 133
 DB 61 KCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHICYGFGIPIIL 120
 QY 134 LTDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASVPGIIFTKCKEDSVYVCGPY 193
 DB 121 LTDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASVPGIIFTKCKEDSVYVCGPY 180
 QY 194 FPRGWNFHTIMRNILGLVPLIMVICYSIGILKTLRCNEKKRHRVAVITIMIVYF 253
 DB 181 FPRGWNFHTIMRNILGLVPLIMVICYSIGILKTLRCNEKKRHRVAVITIMIVYF 240
 QY 254 LFWTYPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFR 313
 DB 241 LFWTYPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCINPIIYAFVGEKFR 300
 QY 314 RYLSVFRKHITKRCQKCVFRETVDGVTSTNTPSTGQEVSA 360
 DB 301 RYLSVFRKHITKRCQKCVFRETVDGVTSTNTPSTGQEVSA 347

RESULT 12
 AAR79165
 ID AAR79165 standard; protein; 374 AA.
 AC AAR79165;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-DEC-1995 (first entry)
 XX
 DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.
 DE Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..48
 FT /label= extracellular
 FT Domain 49..70
 FT /label= transmembrane
 FT Domain 80..700
 FT /label= transmembrane
 FT Domain 115..136
 FT /label= transmembrane
 FT Domain 154..178
 FT /label= transmembrane
 FT Domain 204..231
 FT /label= transmembrane
 FT Domain 244..268
 FT /label= transmembrane
 FT Domain 295..313
 FT /label= transmembrane
 FT Region 314..375
 FT /label= carboxyl tail
 XX
 PN WO9519436-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 11-JAN-1995; 95WO-US000476.
 XX
 PR 13-JAN-1994; 94US-00182962.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Charo I, Coughlin S;
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

DR WPI; 1995-263866/34.
 DR N-PSDB; AAQ96297.
 PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 PT for identifying antagonists and for treating diseases characterised by
 PT monocytic infiltrates.
 XX
 PS Claim 2; Fig 1; 84pp; English.
 XX
 CC To identify and clone new members of the chemokine receptor gene family,
 CC degenerate oligo primers were designed corresp. to the conserved
 CC sequences R79167 in the second and R79168 in the third transmembrane
 CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
 CC HUMSTRS orphan receptor (GenBank Accession #M99293). The degenerate oligo
 CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
 CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
 CC yielded a number of PCR products. One cDNA appeared to encode a novel
 CC protein. To obtain a full-length version of this clone, a MM6 cDNA
 CC library was constructed in pFROG and probed with the PCR product. A 2.1
 CC kb cDNA clone was obt'd. Analysis of additional clones in the MM6 cDNA
 CC library revealed a second sequence that was identical to the 2.1 kb cDNA
 CC sequence first obt'd. from the 5' UTR through the putative seventh
 CC transmembrane domain but contained a different cytoplasmic tail. The
 CC second sequence appears to represent alternative splicing of the carboxyl
 CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
 CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-
 CC 1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
 CC wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 2; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3.1e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
 QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLVSLVIFGVGN 60
 DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGQALLPPLVSLVIFGVGN 60
 QY 61 MLVVLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 DB 61 MLVVLILINCKKLKCLTDIYLLNLAISSDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180
 DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVTSVITLWVAVPASVPGIIFTK 180
 QY 181 CQKEDSVYVCGPYFPRGWNFHTIMRNILGLVPLIMVICYSIGILKTLRCNEKKRHR 240
 DB 181 CQKEDSVYVCGPYFPRGWNFHTIMRNILGLVPLIMVICYSIGILKTLRCNEKKRHR 240
 QY 241 AVRVIPTIMIVYFPLFWTPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFPLFWTPYVILLNTFQFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
 QY 301 NPIIYAFVGEKFRYLSVFPFRKHITKRCQKCV 334
 DB 301 NPIIYAFVGEKFR---SLP---HIALG-CRIAPL 327

RESULT 13
 AAG80107
 ID AAG80107 standard; protein; 374 AA.
 AC AAG80107;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CCR2a protein.
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;

KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 OS Homo sapiens.
 XX WO200172830-A2.
 XX 04-OCT-2001.
 XX 02-APR-2001; 2001WO-EP003708.
 XX 31-MAR-2000; 2000DE-01016013.
 XX (IPFP-) IPF PHARM GMBH.
 XX (FORS/) FORSSMANN U.
 XX Forsemann W, Adermann K, Heitland A, Spodeberg N;
 XX WPI; 2001-626256/72.
 XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX Disclosure; Page 9; 26pp; German.
 XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AA80045-AGA80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 374 AA;
 Query Match 86.9%; Score 1651.5; DB 4; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3.1e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
 QY 1 MLSTSRFRFRNTNESGEVTFDFYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRFRFRNTNESGEVTFDFYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
 QY 61 MLVLLILINCKKLCITDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 DB 61 MLVLLILINCKKLCITDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFFTLLITDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
 DB 121 HIGYFGGIFFTLLITDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180
 QY 181 COKEDSVVCGPYPRGNWFFHTMRNLGLVLPVLLIMVICYSGILKTLRCRNEKKRRH 240
 DB 181 COKEDSVVCGPYPRGNWFFHTMRNLGLVLPVLLIMVICYSGILKTLRCRNEKKRRH 240
 QY 241 AVRVIPTIMIVYFLWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVTTGLMTHCCI 300
 DB 241 AVRVIPTIMIVYFLWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVTTGLMTHCCI 300
 QY 301 NPITIAVGEKFRYLSVFFPKHITKRFKQCPV 334
 DB 301 NPITIAVGEKFRYLSVFFPKHITKRFKQCPV 334
 DB 301 NPITIAVGEKFRYLSVFFPKHITKRFKQCPV 334

RESULT 14
 ABU09083
 ID ABU09083 standard; protein; 374 AA.
 XX
 AC ABU09083;
 XX
 DT 23-JUL-2003 (first entry)
 XX
 DE Human chemokine receptor-2 (CKR-2) polypeptide.
 XX
 KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;
 KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;
 KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;
 KW abnormal physiology; abnormal proliferation; degeneration; atrophy;
 KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.
 XX
 OS Homo sapiens.
 XX
 XX US2003018167-A1.
 XX 23-JAN-2003.
 XX
 XX 03-JAN-2002; 2002US-00039659.
 XX
 XX 05-JUL-1996; 96US-0021664P.
 XX 11-OCT-1996; 96US-0028329P.
 XX 04-JUN-1997; 97US-0048593P.
 XX 03-JUL-1997; 97US-00887977.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
 XX WPI; 2003-416900/39.
 XX
 XX New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful
 PT for treating conditions associated with abnormal physiology or
 PT development, including inflammatory conditions (e.g. asthma), and
 PT abnormal proliferation.
 XX
 PS Disclosure; Page 9-10; 54pp; English.
 XX
 XX The invention relates to nucleic acids encoding the chemokines TECK, MIP-
 CC 3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are
 CC useful in isolating DNA clones encoding the chemokines, for generating
 CC antibodies, and for predicting oligonucleotides for screening a library
 CC to isolate species variants. A nucleic acid encoding a chemokine
 CC polypeptide can be used to identify genes, mRNA and cDNA species which
 CC encode related or homologous ligands, as well as DNA encoding homologous
 CC proteins from different species. The chemokines and antibodies which bind
 CC to the polypeptides are useful in the treatment of conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions such as asthma, abnormal proliferation, regeneration,
 CC degeneration and atrophy. This sequence represents the human chemokine
 CC receptor-2 (CKR-2) polypeptide, used in the scope of the invention
 XX
 SQ Sequence 374 AA;
 Query Match 86.9%; Score 1651.5; DB 6; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3.1e-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
 QY 1 MLSTSRFRFRNTNESGEVTFDFYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
 DB 1 MLSTSRFRFRNTNESGEVTFDFYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
 QY 61 MLVLLILINCKKLCITDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 DB 61 MLVLLILINCKKLCITDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 QY 121 HIGYFGGIFFTLLITDRYLAIVHAVFALKARTVTFGVTSVITWLVAVFASVPGIIFTK 180

Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVPLLMVICYSGILKTLRCNEKKRHR 240
 Db 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVPLLMVICYSGILKTLRCNEKKRHR 240
 Qy 241 AVRVIETIMIVYFLWTPYNNIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300
 Db 241 AVRVIETIMIVYFLWTPYNNIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPV 334
 Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

RESULT 15
 ADD44861
 ID ADD44861 standard; protein; 374 AA.
 XX AC ADD44861;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein P41597, SEQ ID NO 10292.
 XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.
 XX W2003016475-A2.
 XX PD 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 WPI; 2003-268312/26.
 DR GENBANK; P41597.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 374 AA;

Query Match 86.9%; Score 1651.5; DB 7; Length 374;
 Best Local Similarity 95.5%; Pred. No. 3.le-178;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
 Qy 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLLPPLSLVIFGPGVN 60
 Db 1 MLSTSRSRFIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLLPPLSLVIFGPGVN 60
 Qy 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 Db 61 MLVVLILINCKKLKCLTDIYLLNLAIISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
 Qy 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180
 Db 121 HIGYFGGIFPIILLTIDRYLAIVHAFVPAKARTVTFGWTSVITLWVAFASVPGIIFTK 180
 Qy 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVPLLMVICYSGILKTLRCNEKKRHR 240
 Db 181 CQKEDSVYVCGPYPPRGWNNFHTMRNIGLVPLLMVICYSGILKTLRCNEKKRHR 240
 Qy 241 AVRVIETIMIVYFLWTPYNNIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300
 Db 241 AVRVIETIMIVYFLWTPYNNIVLLNTFQFFGLSNCESTSOLDQATQVETLGMTHCCI 300
 Qy 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPV 334
 Db 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327

Search completed: June 9, 2005, 16:44:16
 Job time : 112.826 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:29:43 ; Search time 25.0136 Seconds
(without alignments)
1384.767 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRGRFIRNTNESGEV.....DGVSTNTPSTGGEVSAAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1900 | 100.0 | 360 | 2 JC2443 | chemokine (C-C) re |
| 2 | 1651.5 | 86.9 | 374 | 2 I38450 | chemokine (C-C) re |
| 3 | 1364 | 71.8 | 352 | 2 A43113 | chemokine (C-C) re |
| 4 | 1036 | 54.5 | 355 | 2 A45177 | chemokine (C-C) re |
| 5 | 1010.5 | 53.2 | 359 | 2 I49341 | MIP-1 alpha recept |
| 6 | 963.5 | 50.7 | 355 | 2 I49339 | macrophage inflamm |
| 7 | 951 | 50.1 | 355 | 2 G02436 | chemokine (C-C) re |
| 8 | 871 | 45.8 | 360 | 2 JC4587 | chemokine (C-C) re |
| 9 | 862.5 | 45.4 | 360 | 2 A57160 | chemokine (C-C) re |
| 10 | 822.5 | 43.3 | 383 | 2 S55594 | G protein-coupled |
| 11 | 778.5 | 41.0 | 356 | 2 I49340 | MIP-1 alpha recept |
| 12 | 751 | 39.5 | 355 | 2 JC5067 | G protein-coupled |
| 13 | 722.5 | 38.0 | 354 | 2 I58186 | G protein-coupled |
| 14 | 708 | 37.3 | 355 | 2 JC4304 | orphan G protein-c |
| 15 | 649.5 | 34.2 | 344 | 2 JC5942 | chemokine receptor |
| 16 | 581.5 | 30.6 | 378 | 2 B55735 | lymphocyte-specifi |
| 17 | 569 | 29.9 | 378 | 2 A55735 | G protein-coupled |
| 18 | 567.5 | 29.9 | 378 | 2 A55680 | G protein-coupled |
| 19 | 563 | 29.6 | 369 | 2 JC5068 | G protein-coupled |
| 20 | 547 | 28.8 | 360 | 2 A53611 | interleukin-8 rece |
| 21 | 540.5 | 28.4 | 355 | 2 J01231 | interleukin-8 rece |
| 22 | 540.5 | 28.4 | 359 | 2 A48921 | interleukin-8 rece |
| 23 | 536.5 | 28.2 | 358 | 2 A53752 | interleukin-8 rece |
| 24 | 532.5 | 28.0 | 356 | 2 A52096 | interleukin-8 rece |
| 25 | 532 | 28.0 | 367 | 2 JB0349 | interferon-inducib |
| 26 | 528.5 | 27.8 | 333 | 2 I65989 | G protein-coupled |
| 27 | 528.5 | 27.8 | 350 | 2 A39445 | interleukin-8 rece |
| 28 | 515.5 | 27.1 | 352 | 2 G00048 | fusin (LSTR) - c |
| 29 | 515 | 27.1 | 353 | 2 S28787 | neuropeptide Y/pep |

ALIGNMENTS

RESULT 1

JC2443

Chemokine (C-C) receptor 2, splice form B - human

NrAlternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem

C:Species: Homo sapiens (man)

C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: JC2443; I38463

R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.

Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994

A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prote

A:Reference number: JC2443; MUID:94324942; PMID:8048929

A:Accession: JC2443

A:Molecule type: mRNA

A:Residues: 1-360 <YAM>

A:Cross-references: UNIPROT:P41597; DBJ:D29984; NID:G531246; PIDN:BAA06253.1; PID:G53124

R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot

A:Reference number: A53477; MUID:94195821; PMID:8146186

A:Accession: I38463

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-360 <RES>

A:Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558

C:Genetics:

A:Gene: GDB:CMKBR2

A:Cross-references: GDB:337364; OMIM:601267

A:Map position: 3p21-3p21

C:Superfamily: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane

C:Keywords: vertebrate rhodopsin

F:43-70/Domain: transmembrane #status predicted <TM1>

F:81-100/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:154-178/Domain: transmembrane #status predicted <TM4>

F:207-226/Domain: transmembrane #status predicted <TM5>

F:244-268/Domain: transmembrane #status predicted <TM6>

F:287-309/Domain: transmembrane #status predicted <TM7>

F:14/Binding site: carbohydrate (Aen) (covalent) #status predicted

F:113-130/Bisulfide bonds: #status predicted

Query Match 100.0%; Score 1900; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 1.6e-156;

Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRGRFIRNTNESGEVTFPDYDYGAPCHFDVKQIGAQQLLPPLYSLVFIFGFVGN 60

Db 1 MLSTSRGRFIRNTNESGEVTFPDYDYGAPCHFDVKQIGAQQLLPPLYSLVFIFGFVGN 60

Qy 61 MLVVLILNCKKCLTDIYLLNLAISDLLPLTLPLWAHSAANWVFGNAWCKLFTGLY 120

Db 61 MLVVLILNCKKCLTDIYLLNLAISDLLPLTLPLWAHSAANWVFGNAWCKLFTGLY 120

neuropeptide Y/pep
G protein-coupled
angiotensin II rec
angiotensin II rec
angiotensin II rec
G protein-coupled
angiotensin II rec
angiotensin II rec
angiotensin II rec
angiotensin II rec
angiotensin II rec
angiotensin II rec
angiotensin II rec
angiotensin II rec
G protein-coupled
MDR15 protein - h
G protein-coupled

30 512.5 27.0 352 2 A45747
31 495.5 26.1 350 2 JN0621
32 486.5 25.6 359 2 S15403
33 480.5 25.3 359 2 A42656
34 480 25.3 374 2 S42628
35 475.5 25.0 359 2 JC2134
36 474.5 25.0 359 2 JC1104
37 474.5 25.0 359 2 S44425
38 472.5 24.9 359 2 JH0621
39 471.5 24.8 359 2 J01516
40 469.5 24.7 359 2 JC1194
41 468.5 24.7 359 2 I51372
42 466 24.5 359 2 A48857
43 465.5 24.5 374 2 S32785
44 465 24.5 327 2 S56162
45 465 24.5 372 2 S26667

121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 181 COKEDSVVCGPYFPGWNNFHTIMRNILGLVPLLLMWICYSGLIKTLRCRNEKKRRH 240
 181 COKEDSVVCGPYFPGWNNFHTIMRNILGLVPLLLMWICYSGLIKTLRCRNEKKRRH 240
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQAQVTTETLGMTHCCI 300
 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQAQVTTETLGMTHCCI 300
 301 NPIIYAVGKPRRYLSVFFRKHTKRCQCPVYFRETVDGVTSVTPSTGEOVSAGL 360
 301 NPIIYAVGKPRRYLSVFFRKHTKRCQCPVYFRETVDGVTSVTPSTGEOVSAGL 360

RESULT 2
 I38450
 Chemokine (C-C) receptor 2, splice form A - human
 N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
 C;Species: Homo sapiens (man)
 C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
 C;Accession: I38450
 R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A;Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
 A;Reference number: A53477; MUID:94195821; PMID:8146186
 A;Accession: I38450
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-374 <RES>
 A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:G472555; PIDN:AAA19119.1; PID:G4725
 C;Genetics:
 A;Gene: GDB:CMKBR2
 A;Cross-references: GDB:337364; OMIM:601267
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
 F;44-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;154-178/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;244-265/Domain: transmembrane #status predicted <TM6>
 F;292-309/Domain: transmembrane #status predicted <TM7>
 F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;32-277,113-190/disulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;
 Best Local Similarity 95.5%; Pred. No. 4.8e-135;
 Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

Qy 1 MLSTSRSFIRNTNSESBEVTFPDYDGAPCHKPDVKQIGAOQLLPYLSVIFVFGVGN 60
 Db 1 MLSTSRSFIRNTNSESBEVTFPDYDGAPCHKPDVKQIGAOQLLPYLSVIFVFGVGN 60
 Qy 61 MLVLLILNCKKLKCLTDIYLNLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 Db 61 MLVLLILNCKKLKCLTDIYLNLNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
 Qy 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Db 121 HIGVFGGIFPIILLTIDRYLAIVHVPALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
 Qy 181 COKEDSVVCGPYFPGWNNFHTIMRNILGLVPLLLMWICYSGLIKTLRCRNEKKRRH 240
 Db 181 COKEDSVVCGPYFPGWNNFHTIMRNILGLVPLLLMWICYSGLIKTLRCRNEKKRRH 240
 Qy 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQAQVTTETLGMTHCCI 300
 Db 241 AVRVIPTIMIVYFLFWTPYINIVILLNTFQBFGLSNCESTSOLDQAQVTTETLGMTHCCI 300

Qy 301 NPIIYAVGKPRRYLSVFFRKHTKRCQCPV 334
 Db 301 NPIIYAVGKPR---SLF---HIALG-CRIAPL 327

RESULT 3
 A43113
 Chemokine (C-C) receptor 5 - human
 N;Alternate names: C-C CKR-5; CCR5
 C;Species: Homo sapiens (man)
 C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
 C;Accession: A43113; S71808; A58832; G02653; A58833
 R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
 Biochemistry 35, 3362-3367, 1996
 A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
 A;Reference number: A43113; MUID:96241590; PMID:8639485
 A;Accession: A43113
 A;Molecule type: mRNA
 A;Residues: 1-352 <SAM1>
 A;Cross-references: GB:X91492; NID:G1262810; PIDN:CAA62796.1; PID:G1262811
 R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti
 M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
 Nature 382, 722-725, 1996
 A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
 A;Reference number: S71808; MUID:96345670; PMID:8751444
 A;Accession: S71808
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 182-206;207-230 <SAM2>
 A;Accession: A58834
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-184,'IKDSHLGAGPAAAGHLLGNPKNSASVSK' <SAM3>
 A;Cross-references: GB:X99393; NID:G1524062; PIDN:CAA67767.1; PID:G1524063
 A;Note: This frameshift mutation results in a non-functional receptor but confers a degra
 nd may have had a selective advantage by conferring resistance to Yersinia plague infecti
 R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
 J. Leukoc. Biol. 60, 147-152, 1996
 A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
 A;Reference number: A58832; MUID:96295970; PMID:8699119
 A;Accession: A58832
 A;Molecule type: mRNA
 A;Residues: 1-352 <COM1>
 A;Cross-references: GB:U57840; NID:G1502408; PIDN:AAB17071.1; PID:G1502409
 A;Experimental source: Clone 8, endotoxin-stimulated peripheral blood monocytes
 R;Combadiere, C.
 submitted to the EMBL Data Library, May 1996
 A;Reference number: H01541
 A;Accession: G02653
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-89,'L',91-352 <COM2>
 A;Cross-references: EMBL:U57840
 R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
 J. Biol. Chem. 271, 17161-17166, 1996
 A;Title: Molecular cloning and functional characterization of a novel human CC chemokine
 A;Reference number: A58833; MUID:96291862; PMID:8663314
 A;Accession: A58833
 A;Molecule type: mRNA
 A;Residues: 1-352 <RAP>
 A;Cross-references: GB:U54994; NID:G1457945; PIDN:AAC50598.1; PID:G1457946
 C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
 C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
 C;Genetics:
 A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
 A;Cross-references: GDB:1230510; OMIM:601373
 A;Map position: 3p21-3p21
 C;Function:
 A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
 A;Note: probably acts to control granulocyte proliferation and differentiation
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
 F;32-56/Domain: transmembrane #status predicted <TM1>

```
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Aen) (covalent) #status predicted
F;24-273,106-183/Diculfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match          54.5%; Score 1036; DB 2; Length 355;
Best Local Similarity 56.4%; Pred. No. 6.4e-82;
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

QY      12 NTNSESSEVTFPPDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGFVGNMLVLILINCK 71
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
5 NITED-YDTTDEYDGATPCQKNERAFGAQLLPPLYSLVFVIGLVGNLIVLVLVOYK 63

QY      72 KUKCLTDIYLNLAIISDLLFLITPLWA-HSAANWVFNGMCKLTGLYHIGYFGGIF 130
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
64 RLKNMTSIYLLNLAIISDLLFLFTLPWDIKDDWVFGDMCKILSGPYTTGLYSEIFF 123

QY      131 IILLITDRYLAIHVAFPAFKARTVTGVTSVITWLVAVPASVPGIIFFTKCKEDSVVC 190
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
124 IILLITDRYLAIHVAFPAFKARTVTGVTSIIWALAILASMPGLYFSKTOWEFTHTC 183

QY      191 GPVFP-----RGWNPFTHIMRNILGPLLIMVICYSGILKLRLCRNEKKRHRAVRVIF 246
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
184 SLHPFHESUREWKLFQALKLNFGLVPLLMICITGIKILLRPNEKK-SKAVRLIP 242

QY      247 TIMIVVLEFWTPNYIVILLNTFOEFFGLSNCESTSOLDQATQTETLGMTHCINPIYA 306
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
243 VIMIIEFLFWTPNLTILISVFQDLFTHECEQSRHLDLAQVTEVIATVTHCCNPVIYA 302

QY      307 FVGEEKRRYLSVFRKHITYRCQCPVRYRETVGDVTSINTSTGEQEVSAG 359
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
303 FVGEREPRKYLRQLFHRRVAHLVKWLPFLSVDRLERVSST-SPSTGEHELISAG 354

RESULT 5
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokini
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49341
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A;Residues: 1-359 >RES>
A;Cross-references: UNIPROT:O8K3M7; EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match          53.2%; Score 1010.5; DB 2; Length 359;
Best Local Similarity 53.5%; Pred. No. 1e-79;
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

QY      10 IRNTNESGEVTFPPDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGFVGNMLVLILIN 69
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
8 IKTVESFE--TTPYEYEWAPCEKVRIKELGSWLLPPLYSLVFIIGLGNMVVLILIK 65

QY      70 CKKLGKCLTDIYLLNLAIISDLLFLITPLWAHSA--NEWVFNGMCKLFTGLYHIGYFGGI 128
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
66 YRKLIQIMTWNIYLFNLAIISDLLFLFTVPFWIHVNLWNEGFGHYMKMSLGSFYLYALYSEI 125

QY      129 PFIIILLITDRYLAIHVAFPAFKARTVTGVTSVITWLVAVPASVPGIIFFTKCKEDSVY 198
DB       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
126 PFIIILLITDRYLAIHVAFPAFKARTVTFTVTSIIWTWLAGLAALPEFIFPHESQDSFGFG 185
```

```

Qy 189 VCGPYFPRG-----WNNEHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKRHRAVRV 244
Db 186 SCSRYPEGEEDSKWRKFAHARNWIFGLALPLLVWVICYSGIITKTLRCPN-KKKYKAIRL 244

Qy 245 IFTIMIVFLFWTPYNIIVILLNTFOEPFGLSNCESTSDQATQVTELTGHTHCINPII 304
Db 245 IFVNIWVFIFWTPYNIIVLLSFAHSTFLETSCQSKHLDLMAQVTEIATHTCCVNEFI 304

Qy 305 YAFVGEKPRRYSVFFRKHTKTRFCQKCPVYRRTV-----DGVSTNTPSTGBOEV 356
Db 305 YAFVGERPRKHLRLFHRNVQ-----FTWENIFQFLPGEENGRTSSVSPSTGBOEI 355

Qy 357 S 357
Db 356 S 356

RESULT 6
149339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49339
R:Gao, J.J.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: UNIPROT:P51675; EMBL:U28404; NID:9881547; PIDN:AAA89153.1; PID:98815
C:Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;
Best Local Similarity 52.3%; Pred. No. 1.2e-75;
Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

Qy 21 TTFDFDYDGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVGNMLVLLINCKKLKCLTDIY 80
Db 13 TTFDFDYGSTPCKTAVRAFGAGLLPPLYSLVIFGFGVGNMLVLLINCKKLKCLTDIY 72

Qy 81 LNLAIISDLLPLITPLWAHSA-HSAANEWFGNMGKLFGLVHIGFVGIFILLITIDRY 139
Db 73 LNLAVSLLVFLTLPLFPIIDYKLDWIFGDAMCKLLSGFYLYGLYSIFILLITIDRY 132

Qy 140 LAIVHAVFALKARTVTGVTSTVITLWAVFASVPGIIFTCKQKEDSVVCGPYFPF--- 195
Db 133 LAIVHAVFALKARTVTGLIISITWAILASMPALYFFKAQWFTHTCTSPHPYKSL 192

Qy 196 RGWNNFHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLF 255
Db 193 KQWKRFOALKNLGLILPLLVMIICYAGIIRILLR-RPSEKKVAVRLIFAITLLPFL 251

Qy 256 WTPYNIIVILLNTFOEPFGLSNCESTSDQATQVTELTGHTHCINPIIYAFVGEKPRY 315
Db 252 WTPYNIIVSVFQDVLFTNQCEQSKHLDLMAQVTEIATHTCCVNPYIIVFVGERFWKY 311

Qy 316 LSVFRKHITKRFCKQCPVYRRTVDGV--TSTNTPSTGBOEV 359
Db 312 LRQLFQRHVAIPLAKWLPFL---SVDQLERTSSISFSTGHEHLSAG 354

```

```

RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
A:Reference number: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272

```

```

A:Accession: G02436
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: UNIPROT:P51677; EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477560
R:Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056; PMID:7622448
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106 'N', 108-275 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:gl1199579; PIDN:AAC50469.1; PID:gl1199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.1
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F:36-70/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.1%; Score 951; DB 2; Length 355;
Best Local Similarity 52.6%; Pred. No. 1.4e-74;
Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

Qy 21 TTFDFDYDGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVGNMLVLLINCKKLKCLTDIY 80
Db 14 TSYDYD-VGGLCEKADTRALMAQFPPLYSLVFTVGLLGNVVMILIKYRLRIMTNY 72

Qy 81 LNLAIISDLLPLITPLWAHSA-ANEWFGNMGKLFGLVHIGFVGIFILLITIDRY 139
Db 73 LNLAIISDLLPLITPLFPIIDYKLDWIFGDAMCKLLSGFYLYGLYSIFILLITIDRY 132

Qy 140 LAIVHAVFALKARTVTGVTSTVITLWAVFASVPGIIFTCKQKEDSVVCGPYFPF--- 196
Db 133 LAIVHAVFALKARTVTGVTSTVITLWAVFASVPGIIFTCKQKEDSVVCGPYFPF--- 192

Qy 197 -GWNFHTIMRNILGLVPLLLIMVICYSGILKTLRLCRNEKKRHRAVRVIFTIMIVYFLF 255
Db 193 YSRHFTLRMTIFCLVPLLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVPFIF 251

Qy 256 WTPYNIIVILLNTFOEPFGLSNCESTSDQATQVTELTGHTHCINPIIYAFVGEKPRY 315
Db 252 WTPYNAIILSSYQILFNGDCERTKHLDLVMLVTEIATHTCCVNPYIIVFVGERFRKY 311

Qy 316 LSVFRKHITKRFCKQCPVYRRTVDGVSTNTPSTGBOEVS 357
Db 312 LRHFFRHLMLHGLRYIPFLPSEKLER-TSSVSFSTADPELS 352

RESULT 8
JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: JC4587
R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>

```

A:Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CRA62372.1; PID:g1167851
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;
Best Local Similarity 47.5%; Pred. No. 1.1e-67;
Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;

QY 10 INTNESGEVTFDDYD-YGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVGNMVLVLI 68
DB 6 VTDITQDETVDVNSYVYFESMPKPCCKGKIGKGFVPLPLYSLVIFGFGVGNMVLVLF 65

QY 69 NCKKLKCLTDIYLLNLAIISDLFLTLPLWAHSAANWFGNAMCKLFTGLYHIGYFGGI 128
DB 66 KYRLKSMTDVYLLNLAIISDLFLVSLPFWGYAADQWVFGGLCKIVSMWVYLVGYSGI 125

QY 129 PFIIILLTDIYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFTKCKEDSVY 188
DB 126 FFIIMSDIRYLAIVHAFSLKARTLYGVITSLITWVAFASVPGIIFTKCKEDSVY 185

QY 189 VCGPYF---PGWNNFHTIMRNILGLVPLLMVICYSIGILKTLRCNEKRRHRAVRVI 245
DB 186 YCKTQVSYNSTWVKVLSLEINVLGILLPLGIMLFWYSMIITLQHCNEKK-NRAVRMI 244

QY 246 FTIMIVYLFPTPNVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCINPIIY 305
DB 245 FGWVVLFGFPTPNVNLVLELVEVLQDCTLERYLDYAIQATETLGFHCCINPVII 304

QY 306 APVGEKFRYLSVFRKHITKR----FCKQCPVFRVETDGVTSNTPTSTGEOE 355
DB 305 PFLGKFRKRYITQLFR---TCRGLVLCKHDFLQVYADSMSSSYTOSTVDHD 355

RESULT 9
A57160
Chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
A:Reference number: A57160; MUID:95370289; PMID:7642634
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POM>
A:Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CRA59743.1; PID:g97145
A:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276,110-187/disulfide bonds: #status predicted
F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.4%; Score 862.5; DB 2; Length 360;
Best Local Similarity 48.7%; Pred. No. 6.1e-67;
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

QY 31 PCHKFDVKQIGAQLLPPLYSLVIFGFGVGNMVLVILINCKKLKCLTDIYLLNLAIISDLL 90
DB 28 PCKEIGKAFGLFPLPLYSLVIFGFGVGNMVLVILVLFKYLKLSMTDVLVNLAIISDLL 87

QY 91 FLITLPLWAHSAANWFGNAMCKLFTGLYHIGYFGGIPIILLTDRYLAIVHAFK 150
DB 88 FVPSLFPFGYAADQWVFGGLCKIMSWMYLFGYSGIIFVNLMSIDRYLAIVHAFSUR 147

QY 151 ARTVTFGVVTSVITLWVAFASVPGIIFTKCKEDSVYVCGPYFPRG---WNNFHTIMRN 207
DB 148 ARTLYGVITSLITWVAFASVPGIIFTKCKEDSVYVCGPYFPRG---WNNFHTIMRN 207

QY 208 ILGLVPLLMVICYSIGILKTLRCNEKRRHRAVRVITIMIVYLFPTPNVILLNT 267
DB 208 ILGLVPLGIMLFCYSMIITLQHCNEKK-NKAVKMFVAVVVLFGFPTPNVILFLET 266

QY 268 FQEPFGLSNCESTSOLDQATQVTTGLMTHCCINPIIYAFVCEKRRYLSVFRKHITKR 327
DB 267 LVELEVLQDCTFERYLDYAIQATETLAFVHCINPIIYFGLGKPRKRYLQLFK---TCR 323

QY 328 ---FCKQCPVFRVETDGVTSNTPTSTGEOBSAGL 360
DB 324 GLFVLCCVGLLIQIYSADTPSSSYTOSTVDHDLDHAL 360

RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S55594
R:Teiford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55594
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:NAC13788.1; PID:g695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;
Best Local Similarity 47.9%; Pred. No. 1.9e-63;
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

QY 4 TSRSRFRINTNESGEVTFDDYD---GAPCHKFDVKQIGAQLLPPLYSLVIFGFGVNM 61
DB 32 TTIASLVPSSTSSDYDDLDVDYVESAPCVKSDTTLAAQVWPALYLLVFLFGLGNI 91

QY 62 LVLLILINCKLKCLTDIYLLNLAIISDLFLTLPLWAH---SAANWFGNAMCKLFTGL 119
DB 92 LWIIVIRYMKIKNLTNMLNLNLAIISDLFLTLPLFWMHYIGMYHDWTFGLSLCKLRGV 151

QY 120 YHIGVGGIPIILLTDRYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFT 179
DB 152 CYMSLYSQVFCILLTVDRYLAIVHAFKARTVFGVTSVITLWVAFASVPGIIFT 211

QY 180 KCQKEDSVYVCGPYF---RGWNNFHTIMRNILGLVPLLMVICYSIGILKTLRCNE 235
DB 212 GHQDDNGRVQCDPVYPMSTNVWRAHVAKVIIMLSLILPLLMVAVCYVVIIRLLAR-RPS 270

QY 236 KRRHRAVRVITIMIVYLFPTPNVILLNTFQBFGLSNCESTSOLDQATQVTTGLM 295
DB 271 KKKYKAIRLEIVINAVFVFTPNVILLNTFTHATLLNLQALSSNLDMLITKTWAY 330

Best Local Similarity 46.2%; Pred. No. 7.4e-55;
Matches 160; Conservative 46; Mismatches 121; Indels 19; Gaps 8;

Qy 24 PDYDGA-PCHKFDVKIQIGALLPPLYSLVFIFGVGNMLVLLILNCKKLCITDIYLL 82
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 13 FEYDDSAEACYLGIIVAFGTIFLSIFSLVPTFGVLGNLVLVALTHSRKSISITDIYLL 72
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 83 NLATSDLLFLITLPLWHAASAAWVFNAMCKLTGLYHGYFGIGFIILLTIDRYLAI 142
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 73 NLALSDLLFVATLPFWTHYLISHHEGLHNAMCKLTAPFFIGFGGIFFITVISIDRYLAI 132
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 143 VHVPALKARVTFTGGVTSVITWLVAFPASVPGIIPFKCKEDSVYVCYPFRGMNFH 202
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 133 VLAANSNNRTVQHGVTSISGVAAAIIIVASPQMFTK-RKDS- --CLGDYPEVLQEIW 188
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 203 TMR-----NILGLVPLLIWICYSGILKTLLRCNEKKGRHRAVRVFTIMIVVFLEWTP 258
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 189 PVRNSENVILGFVPLLIISFCYPRIVRTLFSCKRKA-RAIRLLILVVVFFLEWTP 247
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 259 YNIVILNTFOBFGLNCSESTOLDQATQTETLGHTCCINPIIYAFVGKFRRLYSV 318
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 248 YNIVIFLETIKFYNPFPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAPAGEKFRRLYRH 307
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 319 PFRKHITKRCKQCQPV-----YRETVDGVTSINTPSTGEQEV 357
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 308 LYNKLAV-LCCR-PVHAGFSTESQRSRODSLSSLTHTYSEGGS 351
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 14
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to g
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A:Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:G665580; PIDN:AAA91783.1; PID:G665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 37.3%; Score 708; DB 2; Length 355;
Best Local Similarity 46.8%; Pred. No. 1.3e-53;
Matches 145; Conservative 47; Mismatches 108; Indels 10; Gaps 5;

Qy 18 BEVTFDFDY-DYGACHPKFDVKIQIGALLPPLYSLVFIFGVGNMLVLLILNCKKLCI 76
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 6 ESVTENFEYDDLAEACYIGDIVVFGTVLFISIFSIVFAIGLVGNLILVFPALTNSKKPKSV 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 77 TDIVLLNLAISDLLFLITLPLWHAASAAWVFNAMCKLTGLYHGYFGIGFIILLTI 136
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 66 TDIVLLNLALS DLLFVATLPFWTHYLINKEGLHNAMCKLTAPFFIGFGSIFEITVISI 125
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 137 DRYLIAIHVAFKARTVTFGWTSVITWLVAFPASVPGIIFTKCKEDSVYVCYPFR 196
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

| | | | |
|---|-----|--|-----|
| Db | 126 | DRYLAIVLAAANSMNRNTVQHGVTTISLGVAAAILVAAPQFMFTK-QKENE---CLGDYPE | 181 |
| Qy | 197 | GNWNPHFTIMRNI-----LGLVLPLIMIVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVY | 252 |
| Db | 182 | VLQETWPVLRVNEINFLGFLPLLLIMSYCYFRIIQTLFSCKNHKA-KAIKLILLVVIVP | 240 |
| Qy | 253 | FLFWTPYNNIVILLNTFQEFFGLSNCSTESQLDQATQVTTGLMTHCCINPIIYAFVGEKFP | 312 |
| Db | 241 | FLFWTPYNNVMIFLETKLKYDFPSPCDMRKDLRLALSVTETVAFSHCCCLNPLIYAFAGEKF | 300 |
| Qy | 313 | RRYLSVRRFK 322 | |
| Db | 301 | RRYLYHLGYK 310 | |
| RESULT 15 | | | |
| JC5942 | | | |
| Chemokine receptor - human | | | |
| C:Species: Homo sapiens (man) | | | |
| C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 | | | |
| C:Accession: JC5942 | | | |
| R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Cartet, K.C.; Li, Y. | | | |
| Biochem. Biophys. Res. Commun. 243, 264-268, 1998 | | | |
| A:Title: Cloning and characterization of a novel human chemokine receptor. | | | |
| A:Reference number: JC5942; MUID:98139902; PMID:9473515 | | | |
| A:Accession: JC5942 | | | |
| A>Status: preliminary | | | |
| A:Molecule type: DNA | | | |
| A:Residues: 1-344 <FAN> | | | |
| A:Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:AAC39595.1; | | | |
| C:Superfamily: vertebrate rhodopsin | | | |
| Query Match 34.2%; Score 649.5; DB 2; Length 344; | | | |
| Best Local Similarity 43.0%; Pred. No. 1.4e-48; | | | |
| Matches 128; Conservative 54; Mismatches 99; Indels 17; Gaps 5 | | | |
| Qy | 27 | DYGAPCHKFDVKQIGAOQLPLYSIVFIFFGVGNMLVVLILINCKKLCTDIYLLNLAI | 86 |
| Db | 23 | DEAQCDKIDQAQSAQLPSCSAVFVIGVDNLLVVLIVKYGLKRVENIYLLNLAV | 82 |
| Qy | 87 | SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFILLTIDRYLAIVH-A | 145 |
| Db | 83 | SNLCFLLTLPPWAHAG-----GDPMCKILIGLYFVGLYSETFFNCLLTQVQRYLVFLHKG | 136 |
| Qy | 146 | VPALKARTVTFGVVTSVITMLVAVFASVGLIIFTKCKEDSDSVYCG-----PYFPRG--- | 198 |
| Db | 137 | NFFSARRVRPGGIITSVLAWVTAITLPEYVVVYKPMQEDQKYKCAFSTPFLPADFTFW | 196 |
| Qy | 199 | NNFTIMRNLGLVLLIMIVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVYFLEWTP | 258 |
| Db | 197 | XHFTLTKMNSVLVPLFIFFLVQMRKTL---RFREQRYSFLKVLVAIVVFLMLMAP | 253 |
| Qy | 259 | YNIVILLNTFQEFFGLSNCSTESQLDQATQVTTGLMTHCCINPIIYAFVGEKFRYL | 316 |
| Db | 254 | YNIAFFLSTPKRHPSLGDSCKSYNLKDSVHTIKLIATHCINPLIYAFLDGTFSKYL | 311 |

Search completed: June 9, 2005, 16:49:04
Job time : 27.0136 secg

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:28:38 ; Search time 111.335 Seconds
(without alignments)
1655.798 Million cell updates/sec

Title: US-10-791-166-4

Perfect score: 1900

Sequence: 1 MLSTSRSRFIRNTNSESREV.....DGVSTNTPTSGEVSAGL 360

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|------------|---------------------|
| 1 | 1845 | 97.1 | 360 | 1 | CKR2_MACMU | O18793 macaca mula |
| 2 | 1651.5 | 86.9 | 374 | 1 | CKR2_HUMAN | P41597 homo sapien |
| 3 | 1542 | 81.2 | 373 | 1 | CKR2_RAT | O55193 rattus norv |
| 4 | 1535 | 80.8 | 373 | 1 | CKR2_MOUSE | P51683 mus musculus |
| 5 | 1513 | 79.6 | 373 | 2 | O6YT42 | Q6YT42 sus scrofa |
| 6 | 1403 | 73.8 | 354 | 2 | O6SG28 | Q6SG28 rattus norv |
| 7 | 1396 | 73.5 | 354 | 1 | CKR5_MOUSE | P51682 mus musculus |
| 8 | 1392 | 73.3 | 352 | 2 | O95NC2 | Q95NC2 callicebus |
| 9 | 1386 | 72.9 | 354 | 1 | CKR5_RAT | O08556 rattus norv |
| 10 | 1383 | 72.8 | 352 | 2 | O6YT41 | Q6YT41 sus scrofa |
| 11 | 1377 | 72.5 | 352 | 2 | O6WN96 | Q6WN96 leontopithe |
| 12 | 1376 | 72.4 | 352 | 1 | CKR5_CERTO | O62743 cercopithe |
| 13 | 1376 | 72.4 | 352 | 2 | O71RS2 | Q71RS2 cercopithe |
| 14 | 1375 | 72.4 | 352 | 2 | O77776 | O77776 cercopithe |
| 15 | 1375 | 72.4 | 352 | 2 | O8H2T9 | Q8H2T9 salmistr sci |
| 16 | 1375 | 72.4 | 352 | 2 | O9MZA0 | Q9MZA0 callithrix |
| 17 | 1374 | 72.3 | 352 | 2 | O6WN98 | Q6WN98 callithrix |
| 18 | 1373 | 72.3 | 352 | 2 | O95NE1 | Q95NE1 cercopithe |
| 19 | 1373 | 72.3 | 352 | 2 | O6WN93 | Q6WN93 leontopithe |
| 20 | 1371 | 72.2 | 352 | 1 | CKR5_HYLE | O97883 hylobates l |
| 21 | 1371 | 72.2 | 352 | 2 | O95NC4 | Q95NC4 ateles geof |
| 22 | 1371 | 72.2 | 352 | 2 | O95NC9 | Q95NC9 alouatta ae |
| 23 | 1371 | 72.2 | 352 | 2 | O6WN97 | Q6WN97 cebuella py |
| 24 | 1371 | 72.2 | 352 | 2 | O9Y1T2 | Q9Y1T2 cercopithe |
| 25 | 1370 | 72.1 | 352 | 1 | CKR5_MACFA | P61814 macaca fasc |
| 26 | 1370 | 72.1 | 352 | 1 | CKR5_MACMU | P61813 macaca mula |
| 27 | 1370 | 72.1 | 352 | 1 | CKR5_MACNE | P61815 macaca neme |
| 28 | 1370 | 72.1 | 352 | 1 | CKR5_PANPA | P60574 pan paniscu |
| 29 | 1370 | 72.1 | 352 | 1 | CKR5_PANTR | P56440 pan troglod |
| 30 | 1370 | 72.1 | 352 | 1 | CKR5_PONPA | P61756 pongo pygma |
| 31 | 1370 | 72.1 | 352 | 1 | CKR5_PONPY | O97881 pongo pygma |

| | | | | | | |
|----|------|------|-----|---|------------|--------------------|
| 32 | 1370 | 72.1 | 352 | 2 | Q71TZ2 | Q71TZ2 pongo pygma |
| 33 | 1370 | 72.1 | 352 | 2 | Q71TZ7 | Q71TZ7 macaca nigr |
| 34 | 1370 | 72.1 | 352 | 2 | Q71TZ8 | Q71TZ8 macaca tonk |
| 35 | 1370 | 72.1 | 352 | 2 | Q71TZ9 | Q71TZ9 macaca sini |
| 36 | 1368 | 72.0 | 352 | 1 | CKR5_GORGO | P56439 gorilla gor |
| 37 | 1368 | 72.0 | 352 | 1 | CKR5_LOPAT | P61755 lophocebus |
| 38 | 1368 | 72.0 | 352 | 1 | CKR5_PAPAT | P68469 papio anubi |
| 39 | 1368 | 72.0 | 352 | 1 | CKR5_PAPHA | P68270 papio hama |
| 40 | 1368 | 72.0 | 352 | 2 | O18770 | O18770 pan troglod |
| 41 | 1368 | 72.0 | 352 | 2 | O6WN92 | O6WN92 leontopithe |
| 42 | 1368 | 72.0 | 352 | 2 | O6WN94 | O6WN94 leontopithe |
| 43 | 1368 | 72.0 | 352 | 2 | Q71TZ0 | Q71TZ0 gorilla gor |
| 44 | 1368 | 72.0 | 352 | 2 | Q71TZ1 | Q71TZ1 gorilla gor |
| 45 | 1368 | 72.0 | 352 | 2 | Q71TZ8 | Q71TZ8 cercopithe |

ALIGNMENTS

RESULT 1
CKR2_MACMU
ID CKR2 MACMU STANDARD; PRT; 360 AA.
AC O18793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN Name=CCR2; Synonyms=CMKBR2;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684; DOI=10.1089/089222201750290104;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines;
CC Transduces a signal by increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence=Not described;
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
EMBL; AF013958; AAD11572.1; -
DR InterPro; IPR002237; CC 2 receptor.
DR InterPro; IPR000355; ChmKine_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW Sulfation; Transmembrane.
DOMAIN 1 42 Extracellular (Potential).
FT TRANSMEM 43 70 1 (Potential).

| | | | | | |
|---------------------------|---|-----------------------------------|---|-----------------------------------|--------------------------------------|
| FT | DOMAIN | 71 | 80 | Cytoplasmic (Potential). | |
| FT | TRANSMEM | 81 | 100 | 2 (Potential). | |
| FT | DOMAIN | 101 | 114 | Extracellular (Potential). | |
| FT | TRANSMEM | 115 | 136 | 3 (Potential). | |
| FT | DOMAIN | 137 | 153 | Cytoplasmic (Potential). | |
| FT | TRANSMEM | 154 | 178 | 4 (Potential). | |
| FT | DOMAIN | 179 | 206 | Extracellular (Potential). | |
| FT | TRANSMEM | 207 | 226 | 5 (Potential). | |
| FT | DOMAIN | 227 | 243 | Cytoplasmic (Potential). | |
| FT | TRANSMEM | 244 | 268 | 6 (Potential). | |
| FT | DOMAIN | 269 | 285 | Extracellular (Potential). | |
| FT | TRANSMEM | 286 | 309 | 7 (Potential). | |
| FT | DOMAIN | 310 | 360 | Cytoplasmic (Potential). | |
| FT | CARBOHYD | 14 | 14 | N-linked (GlcNAc. .) (Potential). | |
| FT | MOD RES | 26 | 26 | Sulfo tyrosine (By similarity). | |
| FT | DISULFID | 113 | 190 | By similarity. | |
| SQ | SEQUENCE | 360 AA; | 41139 MW; | 4B2552BCE913FE9F CRC64; | |
| Query Match | | | | | 97.1%; Score 1845; DB 1; Length 360; |
| Best Local Similarity | | | | | 96.9%; Pred. No. 5.le-106; |
| Matches 349; Conservative | | | | | 5; Mismatches 6; Indels 0; Gaps 0; |
| QY | 1 | MLSTSRFIRNTN | SGREVTTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFI | FGFVGN | 60 |
| DB | 1 | MLSTSRFIRNTN | SGREVTTFDDYDYGAPCHKFDVKQIGQALLPPLYSLVFI | FGFVGN | 60 |
| QY | 61 | MLVVLINCKK | KLDTIYLLNLAISDLFLITLPLWAHSAANWFGN | AMCKLFTGLY | 120 |
| DB | 61 | MLVVLINCKK | LSLDTIYLLNLAISDLFLITLPLWAHSAANWFGN | AMCKLFTGLY | 120 |
| QY | 121 | HGYFGGFI | PIILLIDRYLAIVHAFKARTVFGVTSVITLVAFASV | RGIIETK | 180 |
| DB | 121 | HGYLGGFI | PIILLIDRYLAIVHAFKARTVFGVTSVITLVAFASV | RGIIETK | 180 |
| QY | 181 | CKEBSVYVCG | PFYPRGWNFTIMNIGLVPLLIWICVSGILKTL | LCRNEKKHR | 240 |
| DB | 181 | COEEDSVIC | PGFYPRGWNFTIMNIGLVPLLIWICVSGILKTL | LCRNEKKHR | 240 |
| QY | 241 | AVRVFTIM | IVFLFWTPNIVILLNTFOEFGLSNCSTSLDQATQ | VTETLGMTHCCI | 300 |
| DB | 241 | AVRLFTIM | IVFLFWTPNIVILLNTFOEFGLSNCSTSLDQATQ | VTETLGMTHCCI | 300 |
| QY | 301 | NPIIVAFGEK | FRRLYSVFRGHITKFCQCPVFRVVDGVTSTNP | STGEQVSVGL | 360 |
| DB | 301 | NPIIVAFGEK | FRRLYSVFRGHITKFCQCPVFRVVDGVTSTNP | STGEQVSVGL | 360 |
| RESULT 2 | | | | | |
| CKR2 | HUMAN | STANDARD; | PRT; | 374 AA. | |
| AC | P41597; | | | | |
| DT | 01-NOV-1995 | (Rel. 32, Created) | | | |
| DT | 01-NOV-1995 | (Rel. 32, Last sequence update) | | | |
| DT | 25-OCT-2004 | (Rel. 45, Last annotation update) | | | |
| DE | C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2) | | | | |
| DE | (Monocyte chemoattractant protein 1 receptor) (MCP-1-R). | | | | |
| GN | Name=CCR2; Synonyms=CMKBR2; | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RX | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=94195821; PubMed=8146186; | | | | |
| RA | Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J., | | | | |
| RA | Coughlin S.R.; | | | | |
| RT | "Molecular cloning and functional expression of two monocyte | | | | |
| RT | chemoattractant protein 1 receptors reveals alternative splicing of | | | | |
| RT | the carboxyl-terminal tails." | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=94324942; PubMed=8048929; | | | | |

| | | |
|----|--|--|
| RA | Yanagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.; | |
| RT | "cDNA cloning and functional expression of a human monocyte | |
| RT | chemoattractant protein 1 receptor."; | |
| RL | Biochem. Biophys. Res. Commun. 202:1156-1162(1994). | |
| RN | [3] | |
| RP | SEQUENCE FROM N.A. | |
| RX | MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038; | |
| RA | Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.; | |
| RT | "Organization and differential expression of the human monocyte | |
| RT | chemoattractant protein 1 receptor gene. Evidence for the role of the | |
| RT | carboxyl-terminal tail in receptor trafficking."; | |
| RN | J. Biol. Chem. 272:1038-1045(1997). | |
| RN | [4] | |
| RP | SEQUENCE FROM N.A. | |
| RA | McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., | |
| RA | Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., | |
| RA | Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., | |
| RA | Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., | |
| RA | Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., | |
| RA | Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., | |
| RA | Sagripanti J.L.; | |
| RA | Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. | |
| RL | Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. | |
| RN | [5] | |
| RP | SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355. | |
| RA | Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., | |
| RA | Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.; | |
| RT | "SeattlesNPS. NHJBI H66682 program for genomic applications, UW- | |
| RT | FKRC, Seattle, WA (URL: http://pga.gs.washington.edu)."; | |
| RL | Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. | |
| RN | [6] | |
| RP | SULFATION OF TYR-26, AND N-GLYCOSYLATION. | |
| RX | MEDLINE=20501139; PubMed=11046064; | |
| RA | Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V., | |
| RA | Chakravarty L., Kolattukudy P.E.; | |
| RT | "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that | |
| RT | has tyrosine sulfation in a conserved extracellular N-terminal | |
| RT | region."; | |
| RL | J. Immunol. 165:5295-5303(2000). | |
| CC | -I- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines. | |
| CC | Transduces a signal by increasing the intracellular calcium ions | |
| CC | level. Alternative coreceptor with CD4 for HIV-1 infection. | |
| CC | -I- SUBCELLULAR LOCATION: Integral membrane protein. | |
| CC | -I- ALTERNATIVE PRODUCTS: | |
| CC | Event-Alternative splicing; Named isoforms=2; | |
| CC | Name=A; | |
| CC | Isoid=P41597-1; Sequence=Displayed; | |
| CC | Name=B; | |
| CC | Isoid=P41597-2; Sequence=VSP_001893; | |
| CC | -I- PTM: N-glycosylated. | |
| CC | -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. | |
| CC | ----- | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | |
| CC | European Bioinformatics Institute. There are no restrictions on its | |
| CC | use by non-profit institutions as long as its content is in no way | |
| CC | modified and this statement is not removed. Usage by and for commercial | |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | |
| CC | or send an email to license@isb-sib.ch). | |
| CC | ----- | |
| DR | EMBL; U03882; AAA19119.1; - | |
| DR | EMBL; U03905; AAA19120.1; - | |
| DR | EMBL; D29984; BAA06253.1; - | |
| DR | EMBL; U80924; AAC51637.1; - | |
| DR | EMBL; U80924; AAC51636.1; - | |
| DR | EMBL; U95626; AAB57791.1; - | |
| DR | EMBL; U95626; AAB57792.1; - | |
| DR | EMBL; AF545480; AAN16400.1; - | |
| DR | PIR; I38450; I38450. | |
| DR | PIR; JC2443; JC2443. | |
| DR | PDB; 1KAD; Model; A=1-349. | |
| DR | PDB; 1KPI; Model; A=1-349. | |
| DR | Genew; HGNC:1603; CCR2. | |
| DR | MIM; 601267; -. | |

GO: 0005887; C: integral to plasma membrane; TAS.
GO: 0005625; S: soluble fraction; TAS.
GO: 0004950; F: chemokine receptor activity; TAS.
GO: 0019735; P: antimicrobial humoral response (sensu Verte. . .); TAS.
GO: 0006968; P: cellular defense response; TAS.
GO: 0006935; P: chemotaxis; TAS.
GO: 0007204; P: cytosolic calcium ion concentration elevation; TAS.
GO: 0006954; P: inflammatory response; TAS.
GO: 0007259; P: JAK-STAT cascade; TAS.
GO: 0007194; P: negative regulation of adenylate cyclase ac. . .; TAS.
InterPro: IPR002237; CC 2 receptor.
InterPro: IPR000355; Chkine receptor.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm 1; 1.
PRINTS: PR00237; GPCR_RHODOPSIN.
PROSITE: PS00237; G PROTEIN RECEPTOR FL1; 1.
PROSITE: PS00262; G PROTEIN RECEPTOR FL2; 1.
3D-structure: Alternative splicing; G-protein coupled receptor;
Glycoprotein; Polymorphism; Sulfation; Transmembrane.
DOMAIN 1 42 Extracellular (Potential).
TRANSMEM 43 70 1 (Potential).
DOMAIN 71 80 Cytoplasmic (Potential).
TRANSMEM 81 100 2 (Potential).
DOMAIN 101 114 Extracellular (Potential).
TRANSMEM 115 136 3 (Potential).
DOMAIN 137 153 Cytoplasmic (Potential).
TRANSMEM 154 178 4 (Potential).
DOMAIN 179 206 Extracellular (Potential).
TRANSMEM 207 226 5 (Potential).
DOMAIN 227 243 Cytoplasmic (Potential).
TRANSMEM 244 268 6 (Potential).
DOMAIN 269 285 Extracellular (Potential).
TRANSMEM 286 309 7 (Potential).
DOMAIN 310 374 Cytoplasmic (Potential).
CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
MOD_RES 26 26 Sulfotyrosine.
FT 113 190 By similarity.
FT 314 374 VARSPLIC
VARIANT 64 64 /FTID=VAR_014339.
VARIANT 355 355 /FTID=VAR_014340.
SEQUENCE 374 AA; 41914 MW; P865E0D39E74CF0P CRC64;
Query Match 86.9%; Score 1651.5; DB 1; Length 374;
Best Local Similarity 95.5%; Pred. No. 4.2e-94;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;
QY 1 MLSTSRIRNTNSESSEVTFPPDYCAPCKFDVQKQIQAQLLPPLYSLVFFIGVGN 60
DB 1 MLSTSRIRNTNSESSEVTFPPDYCAPCKFDVQKQIQAQLLPPLYSLVFFIGVGN 60
QY 61 MLVLLINCKKLKCLDIYLLNLAISDLLFLITPLWAHSAANEWFGNAMCKLFTGLY 120
DB 61 MLVLLINCKKLKCLDIYLLNLAISDLLFLITPLWAHSAANEWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPILLTIDRYLAIVHAFVAKARTVTFGVVTSVITWLNAVPSVPGIIPTK 180
DB 121 HIGYFGGIFPILLTIDRYLAIVHAFVAKARTVTFGVVTSVITWLNAVPSVPGIIPTK 180
QY 181 CQKEDSVYCGPFPFGWNNFTIMRNILGLVPLLIWICYSGILKTLRCNKKRHR 240
DB 181 CQKEDSVYCGPFPFGWNNFTIMRNILGLVPLLIWICYSGILKTLRCNKKRHR 240
QY 241 AVRVITIMLVPLFVTPVNIIVLLNTFOEPFGLNCSESTSOLOQATVETLGNTHCCI 300
DB 241 AVRVITIMLVPLFVTPVNIIVLLNTFOEPFGLNCSESTSOLOQATVETLGNTHCCI 300
QY 301 NPITIAVFGKEFRRLYSVFRKHITKRCKQCPV 334
DB 301 NPITIAVFGKEFRRLYSVFRKHITKRCKQCPV 334

Qy 301 NPIIYAFVGEKERRYLSVFFRKHITKRFCKQCPV 334

Query Match

81.2%; Score 1542; DB 1; Length 373;

Best Local Similarity 80.0%; Pred. No. 2.3e-87;
Matches 288; Conservative 24; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRNTNTEGSEEVTFDDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGVGN 60
DB 14 ILTSHSLFTRSIQELDEGATTPYDDGEPCHTSVKQIGAWILPPLYSLVFIFFGVGN 73
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120
DB 74 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 133
QY 121 HIGYFGGIFILLITDRYLAIVAHVAFKARTTFFGVVTSVITLVAFAVSGIIFTK 180
DB 134 HIGYFGGIFILLITDRYLAIVAHVAFKARTTFFGVVTSVITLVAFAVSGIIFTK 193
QY 181 COKEDSVVVCPPYPRGNNFHTMRNLGLVLPILIMVICYSGILKTLRCRNEKKRHR 240
DB 194 SEQEDDQHTCGPYPTTWMKNFQTIMRNILSLILPLVNVICYSGLILHTLFCRNEKKRHR 253
QY 241 AVRIFTIMVYFLFWTPYINIVILNTFQEPFGLSNCESTSQLDOATQVTTGLMTHCCI 300
DB 254 AVRILFALMIVYFLFWTPYINIVILNTFQEPFGLSNCESTSQLDOATQVTTGLMTHCCI 313
QY 301 NPITYAFVGEKFRYLSVFFPKHITKRCCKCPVYRETVDGVTSTNTPSTGEQVSVGL 360
DB 314 NPITYAFVGEKFRYLSVFFPKHITKRCCKCPVYRETVDGVTSTNTPSTGEQVSVGL 373

RESULT 4
ID_CKR2 MOUSE STANDARD; PRT; 373 AA.
AC P51683; O61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN Name=Ccr2; Synonyms=Cmkr2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RA "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1 alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;
RA Kurihara T., Bravo R.;
RA "Cloning and functional expression of mCCR2, a murine receptor for the
C-C chemokines JE and FIC.";
RL J. Biol. Chem. 271:11603-11606 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;
RX DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNJR3.3.CO;2-H;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RA "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
RL J. Neurosci. Res. 45:382-391 (1996).
CC -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
chemokines. Transduces a signal by increasing the intracellular
calcium ions level.

-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.
-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; U47035; AAC52453.1; --
EMBL; U51719; AAC52557.1; --
EMBL; U56819; AAC52784.1; --
MGD; MGI:106185; Ccr2.
GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
GO; GO:0019955; P:cytokine binding; IPI.
GO; GO:0016086; P:cellular defense response (sensu Vertebrata); IMP.
GO; GO:0030097; P:hemoopoiesis; IMP.
GO; GO:0006959; P:humoral immune response; IMP.
GO; GO:0006954; P:inflammatory response; IMP.
GO; GO:0019233; P:perception of pain; IMP.
GO; GO:0030334; P:regulation of cell migration; IMP.
InterPro; IPR002237; CC_2_receptor.
InterPro; IPR000355; Chemokine_receptor.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR0237; GPCRHOPOPSN.
PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55 Extracellular (Potential).
FT TRANSMEM 56 83 1 (Potential).
FT DOMAIN 84 93 Cytoplasmic (Potential).
FT TRANSMEM 94 114 2 (Potential).
FT DOMAIN 115 127 Extracellular (Potential).
FT TRANSMEM 128 149 3 (Potential).
FT DOMAIN 150 166 Cytoplasmic (Potential).
FT TRANSMEM 167 191 4 (Potential).
FT DOMAIN 192 219 Extracellular (Potential).
FT TRANSMEM 220 239 5 (Potential).
FT DOMAIN 240 256 Cytoplasmic (Potential).
FT TRANSMEM 257 281 6 (Potential).
FT DOMAIN 282 298 Extracellular (Potential).
FT TRANSMEM 299 322 7 (Potential).
FT DOMAIN 323 373 Cytoplasmic (Potential).
FT DISULFID 126 203 By similarity.
FT CONFLICT 39 39 Y -> H (in Ref. 1).
FT CONFLICT 184 184 A -> G (in Ref. 1).
FT CONFLICT 264 264 V -> G (in Ref. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
Query Match 80.8%; Score 1535; DB 1; Length 373;
Best Local Similarity 79.7%; Pred. No. 6.1e-87;
Matches 287; Conservative 25; Mismatches 48; Indels 0; Gaps 0;

QY 1 MLSTSRFRNTNTEGSEEVTFDDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFFGVGN 60
DB 14 ILTSHSLFTRSIQELDEGATTPYDDGEPCHTSVKQIGAWILPPLYSLVFIFFGVGN 73
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 120
DB 74 MLVVLILINCKKLCITDIYLLNLAIISDLLFLITPLWAHSAANEVFGNACKLFTGLY 133
QY 121 HIGYFGGIFILLITDRYLAIVAHVAFKARTTFFGVVTSVITLVAFAVSGIIFTK 180
DB 134 HIGYFGGIFILLITDRYLAIVAHVAFKARTTFFGVVTSVITLVAFAVSGIIFTK 193
QY 181 COKEDSVVVCPPYPRGNNFHTMRNLGLVLPILIMVICYSGILKTLRCRNEKKRHR 240
DB 194 SEQEDDQHTCGPYPTTWMKNFQTIMRNILSLILPLVNVICYSGLILHTLFCRNEKKRHR 253

```

QY 241 AVRVIETIMIVFLFWTPYINVLNTFQFPGLSNCESTSOLDQATQVTTETIGMTHCCI 300
Db 254 AVRLIFAIMTVYFLFWTPYINVLNTFQFPGLSNCESTSOLDQATQVTTETIGMTHCCI 313
QY 301 NPIIYAFVGEKPRYLSVFRKXHTKRCCKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 360
Db 314 NPVIYAFVGEKPRYLSVFRKXHTKRCCKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 373

RESULT 5
Q6YT42 PRELIMINARY; PRT; 373 AA.
ID O6YT42
AC O6YT42; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
DE 2).
GN Name=CCR2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006185; BAD08648.1; -.
DR EMBL; AP006435; BAD08655.1; -.
DR EMBL; AB119271; BAD12134.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; R-C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR002237; CC 2 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01107; CHEMOKINER2.
DR PROSITE; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ
SEQUENCE 373 AA; 42299 MW; FAE55CA527A34E0 CRC64;

Query Match
Best Local Similarity 78.9%; Pred. No. 1.4e-85;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 1 MUGSRIRNTNSGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
Db 14 VLPTSHSLTWNKGNDEBPTTSYDYSEPCQKTSVQIEALLPPLYSLVFIFFGVGN 73
QY 61 MIAVILINCKKLCITDIYILNLAISDLLFLITPLWAHSAANEVFNAGMKLPTGLY 120
Db 74 LLWLILINCKKLSGNTDIYILNLAISDLLFLITPFWAHYAADQWVFNINCKEFTGLY 133
QY 121 HIGYFGGIFILLTIDRYLAIVHAFALKARTVFGVVTSTVITLVAVFASVPGIIFTK 180
Db 134 HIGYFGGIFILLTIDRYLAIVHAFALKARTVFGVVTSTVITLVAVFASVPGIIFIR 193

```

```

QY 181 CQKEDSVYVCGPYFPFGWNNFHTIMRNILGLVLPLLMIVCYSGILKTLRCNEKRRH 240
Db 194 SOEHSYGACAPYFPPLAWKNFHTIMRSILGLVLPLLMVVCYSGILKTLRCNEKRRH 253
QY 241 AVRVIETIMIVFLFWTPYINVLNTFQFPGLSNCESTSOLDQATQVTTETIGMTHCCI 300
Db 254 AVRLIFAIMTVYFLFWTPYINVLNTFQFPGLSNCKNSQDDQATQVTTETIGLTHCCI 313
QY 301 NPIIYAFVGEKPRYLSVFRKXHTKRCCKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 360
Db 314 NPVIYAFVGEKPRYLSVFRKXHTKRCCKQCPVFYRETVDGVTSTNTSTGQEQVSAGL 373

RESULT 6
Q68G28 PRELIMINARY; PRT; 354 AA.
ID O68G28
AC O68G28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chemokine (C-C) receptor 5.
GN Name=Cmbkr5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078756; AAH78756.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ
SEQUENCE 354 AA; 41081 MW; 4CCB9A9C4EE8585C CRC64;

Query Match
Best Local Similarity 73.8%; Score 1403; DB 2; Length 354;
Matches 284; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

```

| Matches 264; Conservative 30; Mismatches 50; Indels 6; Gaps 2; | |
|--|--|
| Qy | 17 GEEVTTTFDYDY--GAPCHKFDVKQIGQAQLLPPLYSLVFIFGFGVGNMLVLLINCKKJK 74 |
| Db | 5 GSIPTIYIDYSAPCKENKQIAQLLPPLYSLVFIFGFGVGNMWVFLILISCKKJK 64 |
| Qy | 75 CLTDIYLNLAI SLLFLITLPLWAHSAANWFGNAMCKLFTGLYHIGYFGGIFPFIILL 134 |
| Db | 65 SMTDIYLFNLAI SLLFLITLPLFARHAAANWFGNINCKLFTGIYHIGYFGGIFPFIILL 124 |
| Qy | 135 TIDRYLATVHAFKARTVTGVTSTVITLWVAFAVSVPGLIIFTKCKEDSVVVCQPYF 194 |
| Db | 125 TIDRYLATVHAFKARTVNGVITSVTVVAVFVSLPIIFWRSQKESHTCSHPH 184 |
| Qy | 195 P-----RGWNNFHTIMRNILGLVPLIMVICYSGILKTLACRNEKKRHRAVRVIFIMI 250 |
| Db | 185 PRIQRFWKHFQTLKWLILSLPLVNVVICYSGILNTLFCRNEKKRHRAVRLIFAIMI 244 |
| Qy | 251 VYFLFWTPYNIIVILNTQBFGLSNCSESTSQLOQATQVTTGLMTHCCINPIIYAFVGE 310 |
| Db | 245 VYFLFWTPYNIIVLLTTTQEFYGLNCCSSNRLDQAMQVTTGLMTHCCINPIIYAFVGE 304 |
| Qy | 311 KFRYLSVFFRKHTKCKCPFYRETVDGVTSTNTPSTGEQSVSAGL 360 |
| Db | 305 KFRNYLSVFFRKHIVKRFCKHCSIFQQVNPDRVSSVYTRSTGQEVSTGL 354 |
| RESULT 7 | |
| CKR5_MOUSE STANDARD; PRT: 354 AA. | |
| AC | P51682; O35313; O35891; P97308; P97405; Q61867; |
| DT | 01-OCT-1996 (Rel. 34, Created) |
| DT | 15-JUL-1998 (Rel. 36, Last sequence update) |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) |
| DE | C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1 alpha receptor). |
| GN | Name=Ccr5; Synonyms=Cmkbr5; |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=129/SvJ; TISSUE=Spleen; |
| RC | MEDLINE=96205938; PubMed=86311787; DOI=10.1074/jbc.271.13.7551; |
| RA | Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L., |
| RA | Charo I.F.; Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1 alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9." |
| RL | J. Biol. Chem. 271:7551-7558(1996). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C57BL/6 X CBA; TISSUE=Thymus; |
| RC | MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445; |
| RA | Meyer A., Coyle A.J., Proudfoot A.B.I., Wells T.N.C., Power C.A.; |
| RT | "Cloning and characterization of a novel murine macrophage inflammatory protein-1 alpha receptor." |
| RL | J. Biol. Chem. 271:14445-14451(1996). |
| RN | [3] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=129/Ola; |
| RC | Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.; |
| RL | Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases. |
| RN | [4] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; |
| RC | MEDLINE=98001387; PubMed=9343222; |
| RA | Kuhmann S.E., Platt E.J., Korak S.L., Kabat D.; |
| RT | "Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses." |
| RL | J. Virol. 71:8642-8656(1997). |
| RN | [5] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=129; |
| RC | MEDLINE=97404635; PubMed=9261347; |
| RA | Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H., |
| RA | Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.; |
| RT | "Two distinct CCR5 domains can mediate coreceptor usage by human immunodeficiency virus type 1." |
| RL | J. Virol. 71:6305-6314(1997). |
| RN | [6] |
| RP | SEQUENCE FROM N.A. |
| RC | Guo B., Kuno K., Harada A., Matsushima K.; |
| RL | Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases. |
| CC | -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. |
| CC | -I- SUBCELLULAR LOCATION: Integral membrane protein. |
| CC | -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoietic cell lines. |
| CC | -I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. |
| CC | ----- |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch). |
| CC | ----- |
| DR | EMBL; U47036; AAC52454.1; - |
| DR | EMBL; X94151; CAA63867.1; - |
| DR | EMBL; U68565; AAB37273.1; - |
| DR | EMBL; U83327; AAC53386.1; - |
| DR | EMBL; AF022990; AAC53389.1; - |
| DR | EMBL; AF019772; AAB71183.1; - |
| DR | EMBL; D83648; BAA12024.1; - |
| DR | MGD; MGI:107182; Ccr5. |
| DR | GO; GO:0016493; F:C-C chemokine receptor activity; IDA. |
| DR | GO; GO:0006952; P:defense response; IMP. |
| DR | InterPro; IPR002240; CC 5 receptor. |
| DR | InterPro; IPR003355; Chemkine receptor. |
| DR | InterPro; IPR000276; GPCR_Rhodpsn. |
| DR | Pfam; PF00001; 7tm.1; 1 |
| DR | PRINTS; PR00237; GPCRHOODPSN |
| DR | PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1. |
| DR | PROSITE; PS00262; G-PROTEIN RECEPT_F1_2; 1. |
| DR | PROSITE; PS00262; G-PROTEIN RECEPT_F1_2; 1. |
| KW | G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane. |
| FT | DOMAIN 1 32 Extracellular (Potential). |
| FT | TRANSMEM 33 60 1 (Potential). |
| FT | DOMAIN 61 70 Cytoplasmic (Potential). |
| FT | TRANSMEM 71 91 2 (Potential). |
| FT | DOMAIN 92 104 Extracellular (Potential). |
| FT | TRANSMEM 105 126 3 (Potential). |
| FT | DOMAIN 127 143 Cytoplasmic (Potential). |
| FT | TRANSMEM 144 168 4 (Potential). |
| FT | DOMAIN 169 200 Extracellular (Potential). |
| FT | TRANSMEM 201 220 5 (Potential). |
| FT | DOMAIN 221 237 Cytoplasmic (Potential). |
| FT | TRANSMEM 238 262 6 (Potential). |
| FT | DOMAIN 263 279 Extracellular (Potential). |
| FT | TRANSMEM 280 303 7 (Potential). |
| FT | DOMAIN 304 354 Cytoplasmic (Potential). |
| FT | DISULFID 103 180 By similarity. |
| FT | CARBOHYD 270 270 N-linked (GlcNAc...) (Potential). |
| FT | VARIANT 11 11 I -> S. |
| FT | VARIANT 62 62 K -> R. |
| FT | VARIANT 66 66 V -> M. |
| FT | VARIANT 97 97 I -> V. |
| FT | VARIANT 109 109 V -> L. |
| FT | VARIANT 156 156 V -> A. |
| FT | VARIANT 160 160 P -> S. |
| FT | VARIANT 185 185 P -> L. |

[illegible]

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
alpha receptor).
Name=Ccr5; Synonym=Cmkbr5;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Mistar; TISSUE=Brain;
MEDLINE=98334064; Pubmed=9670989;
DOI=10.1002/(SICI)1097-4547(19980701)53:1<16:;AID-JNR3>3.3.CO;2-0;
A Spiles O., Gournail N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Barger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RT J. Neurosci. Res. 53:16-28(1998).
[2]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=98318173; Pubmed=9655467; DOI=10.1016/S0165-5728(98)00005-8;
Jiang Y., Salafraza M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RA "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RT J. Neuroimmunol. 86:1-12(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; Y12009; CAA72737.1; -;
 EMBL; U77350; AAC03243.1; -;
 RGD; 620596; Cmkbr5.
 InterPro; IPR002240; CC_5_receptor.
 InterPro; IPR000355; Chkline_receptor.
 InterPro; IPR000276; GPCR_Rhodpsn.
 Pfam; PF00001; 7tm 1; 1.
 PRINTS; PR00237; GPCRHHODPSN.
 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 32 Extracellular (Potential).
 FT TRANSMEM 33 60 1 (Potential).
 FT DOMAIN 61 70 2 (Potential).
 FT TRANSMEM 71 91 2 (Potential).
 FT DOMAIN 92 104 3 (Potential).
 FT TRANSMEM 105 126 3 (Potential).
 FT DOMAIN 127 143 Cytoplasmic (Potential).
 FT TRANSMEM 144 168 4 (Potential).
 FT DOMAIN 169 200 Extracellular (Potential).
 FT TRANSMEM 201 220 5 (Potential).
 FT DOMAIN 221 237 Cytoplasmic (Potential).
 FT TRANSMEM 238 262 6 (Potential).
 FT DOMAIN 263 279 Extracellular (Potential).
 FT TRANSMEM 280 303 7 (Potential).
 FT DOMAIN 304 354 Cytoplasmic (Potential).
 FT DISULFID 103 180 By similarity.
 FT CARBOHYD 270 270 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 72.9%; Score 1386; DB 1; Length 354;
 Best Local Similarity 74.9%; Pred. No. 8.5e-78;
 Matches 262; Conservative 30; Mismatches 52; Indels 6; Gaps 2;
 QY 17 GREVTTFDDYD--GAPCHKFDVKQIGALLPPLSLVPIFGVGNMLVLLINCKKLK 74
 Db 5 GSIPYIVYDIDYMSGAPCKVNVKQIAQLPPLSLVPIFGVGNMVFLLISCKKLK 64
 QY 75 CLTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMLKFTGLYHIGYFGGIFILL 134
 Db 65 SMTDIYLFNLAISDLFLTLPLWAHSAANEVFGNIMKFTGLYHIGYFGGIFILL 124
 QY 135 TIDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 194
 Db 125 TIDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 184
 QY 195 -----PRGNNFHTIMNIGLVLPLIMVICYSGILKTLRLCRNEKKHRAVRVFTIMI 250
 Db 185 LHTQYRFKWHFQTLKMWILSLPLLMVVICYSGLILTLFRCKNEKKHRAVRVFTIMI 244
 QY 251 VYFLFTPTNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPLIYAFVGE 310
 Db 245 VYFLFTPTNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPLIYAFVGE 304
 QY 311 KFRYLSVFPFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSTGQEVSAGL 360
 Db 305 KFRYLSVFPFRKHIVRFRCKHSIFQVNPDRVSSVYVTRSTGQEVSTGL 354

RESULT 10
 Q6YT41 PRELIMINARY; PRT; 352 AA.
 AC Q6YT41;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Chemokine (C-C motif) receptor 5 (Chemokine C-C motif eceptor 5).
 GN Name=CCRS;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
 Uenishi H.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AP006185; BAD08649.1; -;
 DR EMBL; AP006435; BAD08656.1; -;
 DR EMBL; AB119272; BAD12135.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR002240; CC_5_receptor.
 DR InterPro; IPR000355; Chkline_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00057; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40227 MW; 7464CB930911C987 CRC64;

Query Match 72.8%; Score 1383; DB 2; Length 352;
 Best Local Similarity 74.5%; Pred. No. 1.3e-77;
 Matches 260; Conservative 33; Mismatches 50; Indels 6; Gaps 2;
 QY 18 EVTTFDDYDYG--APCHKFDVKQIGALLPPLSLVPIFGVGNMLVLLINCKKLK 75
 Db 4 QTSFPYDIDYMSGPECKTNRQIAARLLPPLSLVPIFGVGNMLVLLINCKKLK 63
 QY 76 LTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMLKFTGLYHIGYFGGIFILLT 135
 Db 64 MTDIYLLNLAISDLFLTLPLWAHSAANEVFGNMQFLTGFYFGGIFILLT 123
 QY 136 IDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 195
 Db 124 IDRYLAIHVAHPALKARTVTFGVTSVITLVAVPASVPGIIFTCKQEDSVYVCGPYF 183
 QY 196 RG----WNFHTIMNIGLVLPLIMVICYSGILKTLRLCRNEKKHRAVRVFTIMV 251
 Db 184 SSQYHFKNFQTLKMWILGLVPLLMVVICYSGLILTLRLCRNEKKHRAVRVFTIMV 243
 QY 252 YFLFTPTNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPLIYAFVGE 311
 Db 244 YFLFTPTNIVILLNTFQFGLSNCESTSQLDQATQVTTGLMTHCCINPLIYAFVGE 303
 QY 312 KFRYLSVFPFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSTGQEVSAGL 360
 Db 304 KFRYLSVFPFRKHIVRRFCKCPVQAEAPDRVSSVYVTRSTGQEVSAGL 352

```

RESULT 11
Q6WN96 PRELIMINARY; PRT; 352 AA.
ID AC Q6WN96 STANDARD; PRT; 352 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
DE CC chemokine receptor 5.
GN Name=CCR5; Synonyms=CMKR5;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=085, 087, 089, and isolate 079;
RX MEDLINE=98321155; PubMed=9656999; DOI=10.1006/viro.1998.9174;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage of
RL primary HIV-1, and HIV-2, and HIV-1."
RL Virology 246:113-124 (1998).
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; AF051902; AAC39830.1; -
DR EMBL; AF051903; AAC39831.1; -
DR EMBL; AF051904; AAC39832.1; -
DR EMBL; AF051905; AAC39833.1; -
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chemokine_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Sulfation; Transmembrane.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD RES 3 3
FT MOD RES 10 10
FT MOD RES 14 14
FT MOD RES 15 15
FT VARIANT 2 2
FT VARIANT 3 3
FT VARIANT 25 25
FT VARIANT 100 100

```

```

Query Match 72.5%; Score 1377; DB 2; Length 352;
Best Local Similarity 75.2%; Pred. No. 3e-77;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;
QY 24 PDYDGA--PCHKFDVKQIGQALLPPLYSLVFPGVGNMLVLLINCKLKLCTDIYL 81
DB 10 YDIDYGASEPCRKIDVKQGAHLLPPLYSWVFLGFGVGNMLVLLINCKPKSMIDYL 69
QY 82 LNLALSDLLFLITPLMAHSAANWVFGNAMCKLFTGLYHYGYFGGIFPFIILLITDLYLA 141
DB 70 LNLALSDLLFLITPFWAHYAAGQWDFGNTWCQFLTGLYFGFGIFPFIILLITDLYLA 129
QY 142 IVHAVFALKARTVFGVTSVITMLVAVFASVPGIIFTKCKEDSVYVCGYFPRG---- 197
DB 130 IVHAVFALKARTVFGVTSVITMLVAVFASVPGIIFTRSQEGVHYTCSPHFPFGYQF 189
QY 198 WNNFHTIMRNILGLVPLLIWVICVSGILKTLRCRNEKKRHRVRLFTIMIVVFLPWT 257
DB 190 WNNFALKNVILGLVPLVWVICVSGILKTLRCRNEKKRHRVRLFTIMIVVFLPWA 249
QY 258 PYNIVLLNTQEFGLSNCSSTOLDQATQVETLGNTHCCINPIIVAFVGEKFRYLS 317
DB 250 PYNIVLLNTQEFGLSNCSSTOLDQAMQVETLGNTHCCVNPPIIVAFVGEKFRYLV 309
QY 318 VFRKHITKRCQKCPVYFRTVDGVTNTPTSGEQRVSAGL 360
DB 310 VFRKHIAKCFRCISIFQKEAPERANSVYTRSTGEQISVGL 352

```

RESULT 12
CKR5_CERTO

FT VARIANT 107 L -> V (in isolate 089).
 FT VARIANT 134 V -> G (in isolate 079).
 FT VARIANT 146 V -> L (in isolate 085 and isolate 089).
 FT VARIANT 340 T -> I (in isolate 079).
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 72.4%; Score 1376; DB 1; Length 352;
 Best Local Similarity 76.4%; Pred. No. 3.5e-77;
 Matches 262; Conservative 31; Mismatches 44; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAOQLPPLYSLVFIYFGVGNMLVLLINCKKLCCLTDIYL 81
 Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVFIYFGVGNMLVLLINCKKLSMTDIYL 69
 Qy 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 141
 Db 70 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 129
 Qy 142 IVHAFVFAKARTVTFGVVTSVITLWAVAFASVPGIIFTKQKEDSVVCGPYFP---RG 197
 Db 130 IVHAFVFAKARTVTFGVVTSVITLWAVAFASVPGIIFTRSQREGLHYTCSHPFPYQVQF 189
 Qy 198 WNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVYFLEWT 257
 Db 190 WNFQTLKIVILGLVPLLVNVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVYFLFWA 249
 Qy 258 PYNIVILLNTFQEPFGLNCSSTSDQATQVTTGLMTHCCINPIIYAFVGEKFRYYLS 317
 Db 250 PYNIVILLNTFQEPFGLNCSSTSDQATQVTTGLMTHCCINPIIYAFVGEKFRYYLS 309
 Qy 318 VFFRKHTKFCQCPVYFRETVDGVTSTNTPTSGEQEVSAGL 360
 Db 310 VFFQKHIAKFCCKCSIFQEQASERASSVYTRSTGEQEISVGL 352

RESULT 13
 Q71RS2 PRELIMINARY; PRT; 352 AA.
 AC Q71RS2
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Chemokine receptor CCR5.
 GN Name=CCR5;
 OS Cercocobus torquatus torquatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocobus.
 OX NCBI_TaxID=81944;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21568355; PubMed=11711592;
 RX DOI=10.1128/JVI.75.24.12014-12027.2001;
 RA Beer B.E., Foley B.T., Kuiken C.L., Tooz Z., Goeken R.M., Brown C.R.,
 RA Hu J., St. Claire M., Korber B.T., Hirsch V.M.;
 RT "Characterization of novel simian immunodeficiency viruses from red-
 capped mangabays from Nigeria (SIVrcmNG409 and -NG411).";
 RL J. Virol. 75:12014-12027(2001).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF349682; AAK69684.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000355; Chkline receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 72.4%; Score 1376; DB 2; Length 352;
 Best Local Similarity 76.4%; Pred. No. 3.5e-77;
 Matches 262; Conservative 31; Mismatches 44; Indels 6; Gaps 2;

Qy 24 FDYDY--GAPCHKFDVKQIGAOQLPPLYSLVFIYFGVGNMLVLLINCKKLCCLTDIYL 81
 Db 10 YDIDYTTSEPCQKINVKQIAARLLPPLYSLVFIYFGVGNMLVLLINCKKLSMTDIYL 69
 Qy 82 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 141
 Db 70 LNLAISSLFLITLPLWAHSAANEWFGNAMCKLFTGLYHIGYFGGIFFIILLIDRYLA 129
 Qy 142 IVHAFVFAKARTVTFGVVTSVITLWAVAFASVPGIIFTKQKEDSVVCGPYFP---RG 197
 Db 130 IVHAFVFAKARTVTFGVVTSVITLWAVAFASVPGIIFTRSQREGLHYTCSHPFPYQVQF 189
 Qy 198 WNNFHTIMRNILGLVPLLIWVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVYFLEWT 257
 Db 190 WNFQTLKIVILGLVPLLVNVICYSGLIKTLRCRNEKKHRAVRVIFTIMIVYFLFWA 249
 Qy 258 PYNIVILLNTFQEPFGLNCSSTSDQATQVTTGLMTHCCINPIIYAFVGEKFRYYLS 317
 Db 250 PYNIVILLNTFQEPFGLNCSSTSDQATQVTTGLMTHCCINPIIYAFVGEKFRYYLS 309
 Qy 318 VFFRKHTKFCQCPVYFRETVDGVTSTNTPTSGEQEVSAGL 360
 Db 310 VFFQKHIAKFCCKCSIFQEQASERASSVYTRSTGEQEISVGL 352

RESULT 14
 Q77776 PRELIMINARY; PRT; 352 AA.
 AC Q77776
 DT 01-NOV-1998 (TREMELrel. 08, Created)
 DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Chemokine receptor CCR5.
 GN Name=CCR5;
 OS Cercocobus torquatus torquatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Cercocobus.
 OX NCBI_TaxID=81944;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99059829; PubMed=9841919;
 RX Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M.S., Lu C.Y.,
 RA Aguilar R.F., Ho D.D., Marx P.A.;
 RT "Natural infection of a homozygous delta24 CCR5 red-capped mangabey
 with an Rb-tropic simian immunodeficiency virus.";
 RL J. Exp. Med. 188:2057-2065(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF084004; AAC62472.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000355; Chkline receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.

KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473DD1D3 CRC64;

Query Match 72.4%; Score 1375; DB 2; Length 352;
Best Local Similarity 76.1%; Pred. No. 4e-77;
Matches 261; Conservative 32; Mismatches 44; Indels 6; Gaps 2;

QY 24 FPDY--GAPCHKPDVKQIGAOQLLPYSLVFIQGVGNMVLVILINCKLKCLTDIYL 81
DB 10 YDIDYTSFPCQKINVKQIAARLLPPLYSLVFVGVGNILVILINCKRLKSMTDIYL 69
QY 82 LNLASDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGVFGGIPFIILLTIDRYLA 141
DB 70 LNLASDLLFLTLPPWAHAAQWDFGNTMCQLTGLYFIFGFGIFPIILLTIDRYLA 129
QY 142 IVHAVFALKARTVTGVTSVITWLVAVPASVPGIIFTCKQKEDSVVCGPYFP----RG 197
DB 130 IVHAVFALKARTVTGVTSVITWLVAVPASVPGIIFTCKQKEDSVVCGPYFP----RG 197
QY 198 WNFHTIMNIGLVPLLIWVICYSGILKTLRCNEKKRHRVAVPTIMIVVFLFWT 257
DB 190 WNFHTIMNIGLVPLLIWVICYSGILKTLRCNEKKRHRVAVPTIMIVVFLFWT 257
QY 258 PYNIVILLNTFOEFGSLNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKPRRYS 317
DB 250 PYNIVILLNTFOEFGSLNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKPRRYS 317
QY 318 VFRKHITKRCCKQCFVYFRETVDGVTSTNTSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQKEAPERANSVYTRSTGEQEISVGL 352

RESULT 15
Q8H2T9 PRELIMINARY; PRT; 352 AA.
AC Q8H2T9
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chemokine receptor CCR5 (CC chemokine receptor 5).
GN Name=ccr5;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22174698; PubMed=12186836;
RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World monkey cells occurs primarily at the stage of virus entry."
RL J. Exp. Med. 196;431-445(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA Seanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF52615; AAN14531.1; -;
DR EMBL; AY278742; AAQ20010.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR002240; CC 5 receptor.
DR InterPro; IPR000355; Chmkin receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.

DR PRINTS; PRO0237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER BLUB; UNKNOWN 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40542 MW; 9FC896PB7F074647 CRC64;

Query Match 72.4%; Score 1375; DB 2; Length 352;
Best Local Similarity 75.2%; Pred. No. 4e-77;
Matches 258; Conservative 32; Mismatches 47; Indels 6; Gaps 2;

QY 24 FPDY--GAPCHKPDVKQIGAOQLLPYSLVFIQGVGNMVLVILINCKLKCLTDIYL 81
DB 10 YDIDYTSFPCQKIDVKQMAQLLPYSLVFIQGVGNMVLVILINCKRLKSMTDIYL 69
QY 82 LNLASDLLFLTLPLWAHSAANWVFGNAMCKLFTGLYHIGVFGGIPFIILLTIDRYLA 141
DB 70 LNLASDLLFLTLPPWAHAAQWDFGNTMCQLTGLYFIFGFGIFPIILLTIDRYLA 129
QY 142 IVHAVFALKARTVTGVTSVITWLVAVPASVPGIIFTCKQKEDSVVCGPYFP----RG 197
DB 130 IVHAVFALKARTVTGVTSVITWLVAVPASVPGIIFTCKQKEDSVVCGPYFP----RG 197
QY 198 WNFHTIMNIGLVPLLIWVICYSGILKTLRCNEKKRHRVAVPTIMIVVFLFWT 257
DB 190 WNFHTIMNIGLVPLLIWVICYSGILKTLRCNEKKRHRVAVPTIMIVVFLFWT 257
QY 258 PYNIVILLNTFOEFGSLNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKPRRYS 317
DB 250 PYNIVILLNTFOEFGSLNCESTSOLDQATQVTTGLMTHCCINPIIYAFVGEKPRRYS 317
QY 318 VFRKHITKRCCKQCFVYFRETVDGVTSTNTSTGEQEVSAGL 360
DB 310 VFFQKHIAKRCCKCSIFQKEAPERANSVYTRSTGEQEISVGL 352

Search completed: June 9, 2005, 16:48:08
Job time : 113.835 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2005, 16:37:43 ; Search time 29.9183 Seconds
(without alignments)
898.236 Million cell updates/sec

Title: US-10-791-166-4
Perfect score: 1900
Sequence: 1 MLSTSRFRIRNTNSESSEV.....DGVTSNTPPTGQSVSAGL 360

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-----------------------|-------------------|
| 1 | 1900 | 100.0 | 360 | 1 US-08-450-393A-4 | Sequence 4, Appli |
| 2 | 1900 | 100.0 | 360 | 3 US-08-446-669-4 | Sequence 4, Appli |
| 3 | 1900 | 100.0 | 360 | 3 US-09-045-583-50 | Sequence 50, Appl |
| 4 | 1900 | 100.0 | 360 | 4 US-09-534-185-50 | Sequence 50, Appl |
| 5 | 1900 | 100.0 | 360 | 4 US-09-131-827A-2 | Sequence 2, Appli |
| 6 | 1900 | 100.0 | 360 | 4 US-09-625-573-4 | Sequence 4, Appli |
| 7 | 1900 | 100.0 | 360 | 5 PCT-US95-00476-4 | Sequence 4, Appli |
| 8 | 1900 | 100.0 | 377 | 4 US-09-949-016-11221 | Sequence 11221, A |
| 9 | 1899 | 99.9 | 360 | 4 US-09-131-827A-20 | Sequence 20, Appl |
| 10 | 1894 | 99.7 | 360 | 4 US-09-826-509-473 | Sequence 473, App |
| 11 | 1873 | 98.6 | 360 | 4 US-08-833-752-7 | Sequence 7, Appli |
| 12 | 1873 | 98.6 | 360 | 4 US-09-938-719-7 | Sequence 7, Appli |
| 13 | 1873 | 98.6 | 360 | 4 US-09-939-226B-7 | Sequence 7, Appli |
| 14 | 1849 | 97.3 | 360 | 3 US-09-045-583-51 | Sequence 51, Appl |
| 15 | 1849 | 97.3 | 360 | 4 US-09-534-185-51 | Sequence 51, Appl |
| 16 | 1838 | 96.7 | 374 | 1 US-08-461-244-3 | Sequence 3, Appli |
| 17 | 1651.5 | 86.9 | 374 | 1 US-08-450-393A-2 | Sequence 2, Appli |
| 18 | 1651.5 | 86.9 | 374 | 3 US-08-446-669-2 | Sequence 2, Appli |
| 19 | 1651.5 | 86.9 | 374 | 4 US-10-039-659A-14 | Sequence 14, Appl |
| 20 | 1651.5 | 86.9 | 374 | 4 US-09-625-573-2 | Sequence 2, Appli |
| 21 | 1651.5 | 86.9 | 374 | 5 PCT-US95-00476-2 | Sequence 2, Appli |
| 22 | 1651.5 | 86.9 | 387 | 4 US-09-949-016-11222 | Sequence 11222, A |
| 23 | 1568.5 | 82.6 | 344 | 3 US-08-466-343D-9 | Sequence 9, Appli |
| 24 | 1568.5 | 82.6 | 344 | 4 US-09-502-784A-9 | Sequence 9, Appli |
| 25 | 1473 | 77.5 | 329 | 4 US-09-502-783A-9 | Sequence 9, Appli |
| 26 | 1473 | 77.5 | 329 | 4 US-09-339-912A-9 | Sequence 9, Appli |
| 27 | 1473 | 77.5 | 329 | 4 US-09-195-662A-9 | Sequence 9, Appli |

| | | | | | |
|----|------|------|-----|---------------------|-------------------|
| 28 | 1386 | 72.9 | 354 | 3 US-08-724-984A-2 | Sequence 2, Appli |
| 29 | 1371 | 72.2 | 352 | 3 US-09-517-605-5 | Sequence 5, Appli |
| 30 | 1370 | 72.1 | 352 | 3 US-09-045-583-52 | Sequence 52, Appl |
| 31 | 1370 | 72.1 | 352 | 4 US-09-534-185-52 | Sequence 52, Appl |
| 32 | 1364 | 71.8 | 352 | 3 US-09-087-232A-13 | Sequence 13, Appl |
| 33 | 1364 | 71.8 | 352 | 3 US-08-861-105-14 | Sequence 14, Appl |
| 34 | 1364 | 71.8 | 352 | 3 US-08-575-967A-2 | Sequence 2, Appli |
| 35 | 1364 | 71.8 | 352 | 4 US-08-833-752-5 | Sequence 5, Appli |
| 36 | 1364 | 71.8 | 352 | 4 US-09-796-202-1 | Sequence 1, Appli |
| 37 | 1364 | 71.8 | 352 | 4 US-09-938-719-5 | Sequence 5, Appli |
| 38 | 1364 | 71.8 | 352 | 4 US-08-771-276-2 | Sequence 2, Appli |
| 39 | 1364 | 71.8 | 352 | 4 US-08-771-276-20 | Sequence 20, Appl |
| 40 | 1364 | 71.8 | 352 | 4 US-09-939-226B-5 | Sequence 5, Appli |
| 41 | 1358 | 71.5 | 352 | 4 US-09-826-509-477 | Sequence 477, App |
| 42 | 1356 | 71.4 | 352 | 4 US-09-502-783A-2 | Sequence 2, Appli |
| 43 | 1356 | 71.4 | 352 | 4 US-09-502-784A-2 | Sequence 2, Appli |
| 44 | 1356 | 71.4 | 352 | 4 US-09-339-912A-2 | Sequence 2, Appli |
| 45 | 1356 | 71.4 | 352 | 4 US-09-195-662A-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-450-393A-4

Query Match 100.0%; Score 1900; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRFRIRNTNSESSEVTFDYDGAPCHKFDVKQIGAOQLLPPLYSLVVFIFGVGN 60
Db 1 MLSTSRFRIRNTNSESSEVTFDYDGAPCHKFDVKQIGAOQLLPPLYSLVVFIFGVGN 60

QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
DB 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 2

US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-669-4

Query Match 100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
DB 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360

RESULT 3

US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-50

Query Match 100.0%; Score 1900; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGQALLPPLYSIVTFIFGVGN 60
QY 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

QY 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
QY 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
DB 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
QY 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
DB 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360
DB 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 4

US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; LENGTH: 360 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGN 60
QY 61 MLVVLILINCKGKCLTDIYLLNLAIISDLLFLITPLWHAASANEVFGNACKLFTGLY 120

DB 61 MLVVLILINCKGKCLTDIYLLNLAIISDLLFLITPLWHAASANEVFGNACKLFTGLY 120
QY 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
QY 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
DB 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
QY 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
DB 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360
DB 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 5

US-09-131-827A-2
; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGN 60
DB 1 MLSTSRFRIRNTNESGEEVTFPDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIPIFGVGN 60
QY 61 MLVVLILINCKGKCLTDIYLLNLAIISDLLFLITPLWHAASANEVFGNACKLFTGLY 120
DB 61 MLVVLILINCKGKCLTDIYLLNLAIISDLLFLITPLWHAASANEVFGNACKLFTGLY 120
QY 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
DB 121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
QY 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
DB 181 CQKEDSVVCGPYPRGWNPHHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKHR 240
QY 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
DB 241 AVRVIPTIMIVYFLFTWTPYINIVILLNTFQEFGLSNCESTSOLDQATQVETLGMTHCCI 300
QY 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360
DB 301 NPIIYAFVGEKFRRLYSVFFRKHTTKRCKQCPVYRETVDGVTSTNTPSTGEQEVSA 360

RESULT 6

US-09-625-573-4
; Sequence 4, Application US/09625573
; Patent No. 6730301
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94308-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-625-573-4

Query Match 100.0%; Score 1900; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MLSTSRSRFRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN | 60 |
| DB | 1 | MLSTSRSRFRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN | 60 |
| QY | 61 | MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| DB | 61 | MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| QY | 121 | HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK | 180 |
| DB | 121 | HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK | 180 |
| QY | 181 | CQKEDSVYVCGPFFPRGNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKKRHR | 240 |
| DB | 181 | CQKEDSVYVCGPFFPRGNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKKRHR | 240 |
| QY | 241 | AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| DB | 241 | AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| QY | 301 | NPIIYAFVGEKFRRLYSVFFRKHITKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL | 360 |
| DB | 301 | NPIIYAFVGEKFRRLYSVFFRKHITKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL | 360 |

RESULT 7

PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-4

Query Match 100.0%; Score 1900; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 8.6e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MLSTSRSRFRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN | 60 |
| DB | 1 | MLSTSRSRFRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVIFGPGVN | 60 |
| QY | 61 | MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| DB | 61 | MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY | 120 |
| QY | 121 | HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK | 180 |
| DB | 121 | HIGYFGGIFPIILLTIDRYLAIHVAHFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK | 180 |
| QY | 181 | CQKEDSVYVCGPFFPRGNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKKRHR | 240 |
| DB | 181 | CQKEDSVYVCGPFFPRGNNFHTIMRNILGLVPLLIIMVICYSGILKTLRCKNEKKRHR | 240 |
| QY | 241 | AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| DB | 241 | AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI | 300 |
| QY | 301 | NPIIYAFVGEKFRRLYSVFFRKHITKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL | 360 |
| DB | 301 | NPIIYAFVGEKFRRLYSVFFRKHITKRCFCQCPVYRETVDGVTSTNTPSTGQEVSAGL | 360 |

RESULT 8

US-09-949-016-11221

```
; Sequence 11221, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11221
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11221

Query Match      100.0%; Score 1900; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 9.1e-151;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 18 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 77
Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 78 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 137
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db 138 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 197
Qy 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLINVCYSGILKTLRCRNEKKRHR 240
Db 198 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLINVCYSGILKTLRCRNEKKRHR 257
Qy 241 AVRVIPTIMIVYFLFTWPNYVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 258 AVRVIPTIMIVYFLFTWPNYVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 317
Qy 301 NPITIAFVGEKFRYLSVFFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360
Db 318 NPITIAFVGEKFRYLSVFFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 377

RESULT 9
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 660030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014, 0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; US-09-131-827A-20

Query Match      99.9%; Score 1899; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 1e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Qy 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLINVCYSGILKTLRCRNEKKRHR 240
Db 181 COKEDSVVCGPYPRGWNPHFTIMRNILGLVLLINVCYSGILKTLRCRNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLFTWPNYVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFTWPNYVILLNTFQEFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Qy 301 NPITIAFVGEKFRYLSVFFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360
Db 301 NPITIAFVGEKFRYLSVFFRKHITKRFCKQCPVYRETVDGVTSTNTPSTGEQVSAGL 360

RESULT 10
US-09-826-509-473
; Sequence 473, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-473

Query Match      99.7%; Score 1894; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 2.7e-150;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Db 1 MLSTSRSRFRINTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIQFVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
Db 121 HIGYFGGIFPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
```

QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240
DB 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240
QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AKRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFFRKHTIKRCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
DB 301 NPIIYAFVGEKFRYLSVFFRKHTIKRCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
RESULT 11
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7
Query Match 98.6%; Score 1873; DB 4; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.5e-148;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIQAQLLPPLXSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIQAQLLPPLXSLVFIQFVGN 60
QY 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTGVTSTNTPSTGQEVSAGL 180
DB 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTGVTSTNTPSTGQEVSAGL 180
QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240
DB 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240

QY 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFFRKHTIKRCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
DB 301 NPIIYAFVGEKFRYLSVFFRKHTIKRCKQCPVYRETVDGVTSTNTPSTGQEVSAGL 360
RESULT 12
US-09-938-719-7
; Sequence 7, Application US/09938719
; Patent No. 6692938
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6692938e
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-938-719-7
Query Match 98.6%; Score 1873; DB 4; Length 360;
Best Local Similarity 98.3%; Pred. No. 1.5e-148;
Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIQAQLLPPLXSLVFIQFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIQAQLLPPLXSLVFIQFVGN 60
QY 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVLLILNCKKLKCLTDIYLLNLAI SDLLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTGVTSTNTPSTGQEVSAGL 180
DB 121 HIGYFGGIFIIILLTDIYLAIVHAFKARTVTGVTSTNTPSTGQEVSAGL 180
QY 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240
DB 181 CQKEDSVVCGPYPPRGWNNFHTIMRNILGLVPLLMIVICYSGLKTLRCRNEKKRHR 240

Db 181 CQKEDSVVCGPYPRGWNPHFTIMRNILGLVLPDLLIWIWICYSGLKTLRCRNEKKHR 240

Qy 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

RESULT 13

US-09-939-226B-7

; Sequence 7, Application US/09939226B

; Patent No. 6800447

; GENERAL INFORMATION:

; APPLICANT: Euroscreen S.A.

; APPLICANT: SAMSON, Michel

; APPLICANT: PARMENTIER, Marc

; APPLICANT: VASSART, Gilbert

; APPLICANT: LIBERT, Frederick

; TITLE OF INVENTION: Methods for Identifying Compounds which Bind the Active CCR5 Chem

; TITLE OF INVENTION: Receptor

; FILE REFERENCE: 9409/2023C

; CURRENT APPLICATION NUMBER: US/09/939,226B

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 08/833,752

; PRIOR FILING DATE: 1997-04-09

; PRIOR APPLICATION NUMBER: US 09/626,939

; PRIOR FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: US 08/810,028

; PRIOR FILING DATE: 1997-03-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 7

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (325)..(327)

; OTHER INFORMATION: Xaa = any amino acid

US-09-939-226B-7

Query Match 98.6%; Score 1873; DB 4; Length 360;

Best Local Similarity 98.3%; Pred. No. 1.5e-148;

Matches 354; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVN 60

Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVN 60

Qy 61 MLVVLILINCKKLCCLTDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKLCCLTDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

Db 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

Qy 181 CQKEDSVVCGPYPRGWNPHFTIMRNILGLVLPDLLIWIWICYSGLKTLRCRNEKKHR 240

Db 181 CQKEDSVVCGPYPRGWNPHFTIMRNILGLVLPDLLIWIWICYSGLKTLRCRNEKKHR 240

Qy 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

RESULT 15

RESULT 14

US-09-045-583-51

; Sequence 51, Application US/09045583

; Patent No. 6287805

; GENERAL INFORMATION:

; APPLICANT: Graham, Gerard J. et al.

; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/045,583

; FILING DATE: 20-MAR-98

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: MNI-044

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 51:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 360 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-09-045-583-51

Query Match 97.3%; Score 1849; DB 3; Length 360;

Best Local Similarity 97.2%; Pred. No. 1.5e-146;

Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVN 60

Db 1 MLSTSRSRFIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFGVN 60

Qy 61 MLVVLILINCKKLCCLTDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Db 61 MLVVLILINCKKLCCLTDIYLLNLAISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

Db 121 HIGVFGIFPIILLTIDRYLAIHVAHFALKARTVTFGVTSVITLWVAFASVPGIIFTK 180

Qy 181 CQKEDSVVCGPYPRGWNPHFTIMRNILGLVLPDLLIWIWICYSGLKTLRCRNEKKHR 240

Db 181 CQKEDSVVCGPYPRGWNPHFTIMRNILGLVLPDLLIWIWICYSGLKTLRCRNEKKHR 240

Qy 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Db 241 AVRVIPTIMIVYFLWTPYINIVILLNTFQBFGLSNCESTSQLDQAQVTTETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

Db 301 NPIIYAFVGEKFRYLSVFFRKHITKEFCQKCPVFFYRETVDGVTSTNTPSTGBOEVSAGL 360

US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767ei Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 97.3%; Score 1849; DB 4; Length 360;
Best Local Similarity 97.2%; Pred. No. 1.5e-146;
Matches 350; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MLSTSRFRTRNTNESGEVTTFFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFI FGVGN 60
Db 1 MLSTSRFRTRNTNGSGEVTTFDDYDYGAPCHKFDVKQIGAOQLPPLYSLVFI FGVGN 60
Qy 61 MVLVLILINCKKLCGLTDIYLLNLAIASDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Db 61 MVLVLILINCKKLSLDIYLLNLAIASDLLFLITPLWAHSAANEWVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLITDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Db 121 HIGYLGGIFFIILLITDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
Qy 181 CQEDSVYVCGPYFPRGNFNFTIMRNILGLVLPLLIMVICSYGILKTLRCRNEKKRHR 240
Db 181 CQEDSVYICGPIFFPRGNFNFTIMRNILGLVLPLLIMVICSYGILKTLRCRNEKKRHR 240
Qy 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRLLFTIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTRQLDQATQVTTGLMTHCCI 300
Qy 301 NPITIPVSGKFRRLYSVFRPKHITKRFCKQCPVFRYRETVDGVTSTNTPSTGEQVSAGL 360
Db 301 NPITIPVSGKFRRLYSMFFRKYITKRFCKQCPVFRYRETVDGVTSTNTPSTGEQVSAGL 360

Search completed: June 9, 2005, 16:50:11
Job time : 30.9183 secs


```

Db      61  MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
QY      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
Db      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360
Db      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360

RESULT 2
US-10-225-567A-460
; Sequence 460, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE OF INVENTION: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 460
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-460

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60
Db      1  MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60
QY      61  MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
QY      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
Db      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360
Db      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360

```

RESULT 3
US-10-164-649-50

```

; Sequence 50, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-164-649-50

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60
Db      1  MLSTSRFRIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVIFGFGVN 60
QY      61  MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
Db      61  MLVVLILINCKKLCCLTDIYLLNLAI SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
Db      121  HIGVFGGIFPIILLTIDRYLAI VHAFALKARTVTFGVTSVITLWVAVFASVPGIIFTK 180
QY      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
Db      181  CQKEDSVVCGPYFPPRGWNNFHTIMRNILGLVPLLIWVICYSGILKTLRCNEKKRHR 240
QY      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
Db      241  AVRVITIMIVYFLWTPYNNIVILLNTFQFFGLSNCESTSDQATQVTTETLGMTHCCI 300
QY      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360
Db      301  NPIIYAVGKEKFRYLSVFFRKHTKRFCKQCPVYRETVDGVTSTNTPTSGQEVSAGL 360

```

RESULT 4
US-10-239-423-64

```

; Sequence 64, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:
; APPLICANT: FORSMANN, Wolf-Georg; FORSMANN, Ulf; ADERMAN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammatory Cells and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 64
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-64

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFRFRNTNSESSEVTFDFDYGAPCHKFDVKQIQAQLLPYLSLVFIFGVGN 60
Db 1 MLSTSRFRFRNTNSESSEVTFDFDYGAPCHKFDVKQIQAQLLPYLSLVFIFGVGN 60

Qy 61 MLVLLILNCKKCLDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Db 61 MLVLLILNCKKCLDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy 121 HIGVFGIFPIILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
Db 121 HIGVFGIFPIILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNFHTMRNIGLVLPPLLIMVICYSGILKTLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNFHTMRNIGLVLPPLLIMVICYSGILKTLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVETLGMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYFRETVDGVTSTNTPSTGQEVSAAGL 360
Db 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYFRETVDGVTSTNTPSTGQEVSAAGL 360

```

RESULT 5

```

US-10-439-845-8
; Sequence 8, Application US/10439845
; Publication No. US20030195348A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/864,458
; APPLICATION NUMBER: 08/864,458
; FILING DATE: May 28, 1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-439-845-8

```

```

Query Match      100.0%; Score 1900; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFRFRNTNSESSEVTFDFDYGAPCHKFDVKQIQAQLLPYLSLVFIFGVGN 60
Db 1 MLSTSRFRFRNTNSESSEVTFDFDYGAPCHKFDVKQIQAQLLPYLSLVFIFGVGN 60

Qy 61 MLVLLILNCKKCLDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Db 61 MLVLLILNCKKCLDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120

Qy 121 HIGVFGIFPIILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
Db 121 HIGVFGIFPIILLTIDRYLAIVHAFKARTVTFGVVTSVITLWVAFASVPGIIFTK 180

Qy 181 CQKEDSVYVCGPYFPRGWNFHTMRNIGLVLPPLLIMVICYSGILKTLRCRNEKKRHR 240
Db 181 CQKEDSVYVCGPYFPRGWNFHTMRNIGLVLPPLLIMVICYSGILKTLRCRNEKKRHR 240

Qy 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVETLGMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYNYVILLNTFQBFPGLSNCESTSQLDOATQVETLGMTHCCI 300

Qy 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYFRETVDGVTSTNTPSTGQEVSAAGL 360
Db 301 NPIIYAFVGEKFRYLSVFFRKHTKRFCKQCPVYFRETVDGVTSTNTPSTGQEVSAAGL 360

```

RESULT 6

```

US-10-741-601-285
; Sequence 285, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 360
; TYPE: PRT

```

ORGANISM: Homo sapiens
US-10-741-601-285

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
QY 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
QY 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSGQEVSAGL 360
DB 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSGQEVSAGL 360

RESULT 7
US-10-741-601-286
Sequence 286, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-601-286

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
QY 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240
QY 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300

Db 241 AVRVIETIMIVYFLFWTPYNNIVILLNTFOEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSGQEVSAGL 360
Db 301 NPIIYAFVGEKFRYLSVFRKHITKRFCKQCPVFRVETVDGVTSTNTPTSGQEVSAGL 360

RESULT 8
US-10-791-592-4
Sequence 4, Application US/10791592
Publication No. US20040219644A1
GENERAL INFORMATION:
APPLICANT: Charo, Israel
Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/791,592
FILING DATE: 01-Mar-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/625,573
FILING DATE: 25-Jul-2000
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816C00LEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-791-592-4

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
DB 1 MLSTSRFRIRNTNESGEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLSLVIFGFVGN 60
QY 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKCLTDIYLLNLAISSDLFLITLPLWAHSAANEVWFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTDIYLAIVHAVFALKARTVTFGVVTSVITLWVAVPASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGNNFHTIMRNILGLVPLIMVICYSGILKTLRCNEKKRHR 240

Db 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSILKTLRCNEKKHR 240
Qy 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
Qy 301 NPIIYAVGKPRYLSVFPKRKHITKRFCKQCPVFFRETVDGVTSTNTPTSGEVSAGL 360
Db 301 NPIIYAVGKPRYLSVFPKRKHITKRFCKQCPVFFRETVDGVTSTNTPTSGEVSAGL 360

RESULT 9

US-10-791-166-4
; Sequence 4, Application US/10791166
; Publication No. US20040223968A1
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10791,166
; FILING DATE: 01-Mar-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-791-166-4

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPLPLSLVIFGVGN 60
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPLPLSLVIFGVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAFSPVPGIIFTK 180

Db 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAFSPVPGIIFTK 180
Qy 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSILKTLRCNEKKHR 240
Db 181 CQKEDSVVCGPYPRGNNFHTIMRNILGLVPLLLIMVICYSILKTLRCNEKKHR 240
Qy 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
Db 241 AVRVIPTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSQLDQATQVTTGLMTHCCI 300
Qy 301 NPIIYAVGKPRYLSVFPKRKHITKRFCKQCPVFFRETVDGVTSTNTPTSGEVSAGL 360
Db 301 NPIIYAVGKPRYLSVFPKRKHITKRFCKQCPVFFRETVDGVTSTNTPTSGEVSAGL 360

RESULT 10

US-10-700-313-8
; Sequence 8, Application US/10700313
; Publication No. US20040259785A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10700,313
; FILING DATE: 31-Oct-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,458
; FILING DATE: 28-May-1997
; APPLICATION NUMBER: Provisional 60/018,508
; FILING DATE: May 28, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08830/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-700-313-8

Query Match 100.0%; Score 1900; DB 16; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPLPLSLVIFGVGN 60
Db 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHKFDVKQIGAOQLPLPLSLVIFGVGN 60
Qy 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Db 61 MLVVLILINCKKLCITDIYLLNLAIISDLFLITLPLWAHSAANEVFGNAMCKLFTGLY 120
Qy 121 HIGYFGGIFPIILLTIDRYLAIHVAHPALKARTVTFGVVTSVITLWLVAFSPVPGIIFTK 180

```

121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360
301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360

RESULT 11
US-10-486-471-4
; Sequence 4, Application US/10486471
; Publication No. US20050101530A1
; GENERAL INFORMATION:
; APPLICANT: TOPIGEN PHARMACEUTIQUE INC.
; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE
; FILE REFERENCE: 00953-0003
; CURRENT APPLICATION NUMBER: US/10/486,471
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/311,088
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-486-471-4

```

```

Query Match 100.0%; Score 1900; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
QY 241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360
DB 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360

```

```

RESULT 12
US-10-846-185-8
; Sequence 8, Application US/10846185
; Publication No. US20050118677A1
; GENERAL INFORMATION:
; APPLICANT: Combadiere et al.,
; TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
; NUMBER OF SEQUENCES: 9

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/846,185
FILING DATE: 14-May-2004
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-846-185-8

```

```

Query Match 100.0%; Score 1900; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGALLPPLYSLVFIFGVGN 60
QY 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
DB 121 HIGYFGGIFPIILLTDRYLAIHVAHFALKARTVTFGVVTSVITLWVAFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYFPRGWNFFHIMRNILGLVPLLMVLCYSGILKTLRCRNEKKRHR 240
QY 241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVAVITIMIVYFLFWTPYNNIVILLNTFQEFFGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360
DB 301 NPIIYAFVGEKFRYLSVFFRKHITKRFCKQCPVFRYRETVGVTSNTPTSGQEVSAAGL 360

```

```

RESULT 13
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.

```

```

; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131.827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match          99.9%; Score 1899; DB 9; Length 360;
Best Local Similarity 99.7%; Pred. No. 5.4e-150;
Matches 359; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGGKPRYLSVFRKHIKTRFCQCPVFRYRETVDGVTSTNTPTSGEQVSAGL 360
DB 301 NPIIYAFVGGKPRYLSVFRKHIKTRFCQCPVFRYRETVDGVTSTNTPTSGEQVSAGL 360

RESULT 14
US-09-826-509-473
; Sequence 473, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-473

Query Match          99.7%; Score 1894; DB 10; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.4e-149;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240

US-09-826-509-473

```

```

Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
QY 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSOLDQATQVTTGLMTHCCI 300
DB 241 AVRVFTIMIVYFLFWTPYNNIVILLNTFQBFPGLSNCESTSOLDQATQVTTGLMTHCCI 300
QY 301 NPIIYAFVGGKPRYLSVFRKHIKTRFCQCPVFRYRETVDGVTSTNTPTSGEQVSAGL 360
DB 301 NPIIYAFVGGKPRYLSVFRKHIKTRFCQCPVFRYRETVDGVTSTNTPTSGEQVSAGL 360

RESULT 15
US-10-925-095-473
; Sequence 473, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 473
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-473

Query Match          99.7%; Score 1894; DB 17; Length 360;
Best Local Similarity 99.7%; Pred. No. 1.4e-149;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
DB 1 MLSTSRFRIRNTNSESSEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFFGVGN 60
QY 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
DB 61 MLVVLILINCKKLCCLTDIYLLNLAISSDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
QY 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
DB 121 HIGYFGGIPFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTK 180
QY 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240
DB 181 CQKEDSVYVCGPYPRGWNFNHIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHR 240

US-10-925-095-473

```

| | | | | | |
|----|-----|----------------------|---------------------|------------------------|-----|
| Qy | 241 | AVRVITIMIVYFLEWTPYNI | VILLNTFQEFFGLSNCE | TSQDDQATQVTETLGMTHCCI | 300 |
| Db | 241 | AKRVITIMIVYFLEWTPYNI | VILLNTFQEFFGLSNCE | TSQDDQATQVTETLGMTHCCI | 300 |
| Qy | 301 | NPITYAFVGEKFRYLSVFF | PKKHITKRFCKQCPVFYRE | TVDGVTSTNTPTSTGEQVSAGL | 360 |
| Db | 301 | NPITYAFVGEKFRYLSVFF | PKKHITKRFCKQCPVFYRE | TVDGVTSTNTPTSTGEQVSAGL | 360 |

Search completed: June 9, 2005, 17:06:38
Job time : 101.545 secs